



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking-Number: 206221

TO: Quang Nguyen  
Location: rem/2E81/2C70  
Art Unit: 1633  
Thursday, November 02, 2006  
Case Serial Number: 10/706798

From: Kristine Hensle  
Location: Biotech-Chem Library  
REM-1B69  
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

### Search Notes

Examiner Nguyen,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle  
Librarian (ASRC Aerospace)  
STIC Biotech/Chem Library  
(571)272-4161

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 19:39:18 ; Search time 1837.86 Seconds  
(without alignments)  
2887.948 Million cell updates/sec

Title: US-10-706-798-1

Perfect score: 83  
Sequence: 1 ccuugagguagaagacgacg.....gcugcucuaaauaacaag 83

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_dl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_rts:\*  
8: gb\_ey:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_hcg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_da:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	83	2	CS185098
2	83	100.0	83	2	CS188802
3	83	100.0	663	5	AY866304
4	83	100.0	712	5	AY866308
5	83	100.0	747	5	AY866306
6	83	100.0	825	5	AY866302
7	83	100.0	836	5	AY866299
8	83	100.0	871	5	AY866301
9	83	100.0	896	5	AY866305
10	83	100.0	901	5	AY866300
11	83	100.0	902	5	AY866307
12	83	100.0	914	5	AY866303
13	83	100.0	153092	5	AC069475
14	83	100.0	154868	5	AF334404
15	83	100.0	154887	5	AL137060
16	83	100.0	184155	12	AC155017
17	83	100.0	235659	12	AC152429
18	83	100.0	347503	5	AF279660

C	19	83	100.0	350000	5	AF440619
C	20	79	95.2	108	2	CS188801
C	21	71.8	86.5	172152	6	AC154660
C	22	40	48.2	40	2	CS189094
C	23	40	48.2	40	2	CS189095
C	24	35.8	43.1	150820	12	AC154053
C	25	35.2	42.4	97210	11	AL606727
C	26	35.2	42.4	214290	11	BX294379
C	27	33.4	40.2	83	2	CS185098
C	28	33.4	40.2	83	2	CS188802
C	29	33.4	40.2	663	5	AY866304
C	30	33.4	40.2	712	5	AY866306
C	31	33.4	40.2	747	5	AY866306
C	32	33.4	40.2	825	5	AY866302
C	33	33.4	40.2	836	5	AY866299
C	34	33.4	40.2	871	5	AY866301
C	35	33.4	40.2	896	5	AY866305
C	36	33.4	40.2	901	5	AY866300
C	37	33.4	40.2	902	5	AY866307
C	38	33.4	40.2	914	5	AY866303
C	39	33.4	40.2	153092	5	AC069475
C	40	33.4	40.2	154868	5	AF334404
C	41	33.4	40.2	154887	5	AL137060
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ALIGNMENTS

AF440619	Homo sapi
CS188801	Sequence
AC154660	Mus muscu
CS189094	Sequence
CS189095	Sequence
AC154053	Ictalurus
AL606727	Zebrafish
AX294379	Zebrafish
CS185098	Sequence
CS188802	Sequence
AY866304	Lemur cat
AY866306	Lagotrix
AY866306	Pongo pyg
AY866302	Sagunus
AY866299	Ateles ge
AY866301	Macaca ne
AY866305	Macaca mu
AY866300	Gorilla g
AY866307	Pan trogl
AY866303	Pan panis
AC069475	Homo sapi
AF334404	Homo sapi
AL137060	Human DNA
AC155017	Bos tauru
CR478286	Zebrafish
AC152429	Bos tauru
AF279660	Homo sapi

RESULT 1	CS185098	83 bp	RNA	linear	PAT 01-NOV-2005
LOCUS	CS185098				
DEFINITION	Sequence 72 from Patent WO2005098029.				
ACCESSION	CS185098				
VERSION	CS185098.1	GI:78585070			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Jacobsen, N.				
AUTHORS					
TITLE	NOVEL METHODS FOR QUANTIFICATION OF MICRORNAS AND SMALL INTERFERING				
JOURNAL	Patent: WO 2005098029-A 72 20-OCT-2005;				
FEATURES	Exigun A/S (DK)				
source	1. 83				
ORIGIN	1. 83				
Query Match	100.0%; Score 83; DB 2; Length 83;				
Best Local Similarity	73.5%; Pred. No. 1.4e-20;				
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Qy	61 UGUGCUCGUCUCAAUAAUACAAAG 83				
Db	61 TGTGCTGCTCCTCAAAAATACAAAG 83				
RESULT 2	CS188802	83 bp	DNA	linear	PAT 04-NOV-2005
LOCUS	CS188802				

DEFINITION Sequence 33 from Patent WO2005078139.  
ACCESSION CS188802  
VERSION CS188802.1 GI:80749791  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
1 Croce, C.M.  
AUTHORS Patenc: WO 2005078139-A 33 25-AUG-2005;  
JOURNAL THOMAS JEFFERSON UNIVERSITY (US)  
FEATURES  
source  
1..83  
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Best Local Similarity 73.5%; Pred. No. 1.4e-20;  
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCUUGAGUAAAGUAGCAGACAUAUAGUUUGUGAUUUUGAAAAGUGCAGGCCAUU 60  
Db 1 CCTTGGAGTAAAGTAGCAGACATATGTTGTGGATTGTGAAAAGGTGAGCCCATAT 60  
Qy 61 UUGUCUGCCUCAAANAUAACAAG 83  
Db 61 TGTGCTGCTCAAAAATATCAAG 83  
RESULT 3  
AY866304 663 bp DNA linear PRI 24-JAN-2005  
LOCUS Lemur catca microRNA mir-15a and microRNA mir-16-1 genes, complete  
DEFINITION sequence.  
ACCESSION AY866304  
VERSION AY866304.1 GI:57903106  
KEYWORDS  
SOURCE Lemur catca (ring-tailed lemur)  
ORGANISM Lemur catca  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Strepsithini;  
Lemuridae; Lemur.  
REFERENCE  
1 (bases 1 to 663)  
AUTHORS Berezhikov, E., Guryev, V., van de Belt, J., Wienholds, E.,  
Plasterk, R.H., and Cuppen, E.  
TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE  
2 (bases 1 to 663)  
AUTHORS Berezhikov, E., Guryev, V., van de Belt, J., Wienholds, E.,  
Plasterk, R.H.A. and Cuppen, E.  
TITLE Direct Submission  
JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht  
3584 CT, The Netherlands  
FEATURES  
source  
1..663  
/organism="Lemur catca"  
/mol\_type="genomic DNA"  
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/note="Based on Homo sapiens mir-15a"  
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/product="precursor microRNA mir-16-1"  
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misc\_RNA

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Best Local Similarity 73.5%; Pred. No. 1.6e-20;  
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCUUGAGUAAAGUAGCAGACAUAUAGUUUGUGAUUUUGAAAAGUGCAGGCCAUU 60  
Db 450 CCTTGGAGTAAAGTAGCAGACATATGTTGTGGATTGTGAAAAGGTGAGCCCATAT 509  
Qy 61 UUGUCUGCCUCAAANAUAACAAG 83  
Db 510 TGTGCTGCTCAAAAATATCAAG 532  
RESULT 4  
AY866308 712 bp DNA linear PRI 24-JAN-2005  
LOCUS Lagotrix lagotricha microRNA mir-15a and microRNA mir-16-1 genes,  
DEFINITION complete sequence.  
ACCESSION AY866308  
VERSION AY866308.1 GI:57903110  
KEYWORDS  
SOURCE Lagotrix lagotricha (common woolly monkey)  
ORGANISM Lagotrix lagotricha  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;  
Cebidae; Ateleinae; Lagotrix.  
REFERENCE  
1 (bases 1 to 712)  
AUTHORS Berezhikov, E., Guryev, V., van de Belt, J., Wienholds, E.,  
Plasterk, R.H., and Cuppen, E.  
TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE  
2 (bases 1 to 712)  
AUTHORS Berezhikov, E., Guryev, V., van de Belt, J., Wienholds, E.,  
Plasterk, R.H.A. and Cuppen, E.  
TITLE Direct Submission  
JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht  
3584 CT, The Netherlands  
FEATURES  
source  
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Best Local Similarity 73.5%; Pred. No. 1.6e-20;  
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
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Db 390 CCTTGGAGTAAAGTAGCAGACATATGTTGTGGATTGTGAAAAGGTGAGCCCATAT 449  
Qy 61 UUGUCUGCCUCAAANAUAACAAG 83  
Db 450 TGTGCTGCTCAAAAATATCAAG 472  
RESULT 5

AY866306  
LOCUS AY866306 747 bp DNA linear PRI 24-JAN-2005  
DEFINITION Pongo pygmaeus microRNA mir-15a and microRNA mir-16-1 genes,  
complete sequence.  
ACCESSION AY866306  
VERSION AY866306.1 GI:57903108  
KEYWORDS  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Pongo.  
REFERENCE  
AUTHORS 1 (bases 1 to 747)  
Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H. and Cuppen,E.  
TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE 2 (bases 1 to 747)  
Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H.A. and Cuppen,E.  
AUTHORS Direct Submission  
TITLE Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht  
JOURNAL 3584 CT, The Netherlands  
LOCATION/Qualifiers  
FEATURES  
source 1..747  
/organism="Pongo pygmaeus"  
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/db\_xref="taxon:9600"  
477..559  
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/note="based on Homo sapiens mir-15a"  
490..511  
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617..705  
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630..651  
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Best Local Similarity 73.5%; Pred. No. 1.6e-20;  
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTUGAGUAAAGUAGACACAUAAUGGUAUUUGAAAGGUGAGCCCAU 60  
Db 477 CTTTGAGTAAAGTAGACACATATGCTTTGTGATTGAAAGGTGACGCCATAT 536  
QY 61 UGUGCUGCCUCAAUAUACAAG 83  
Db 537 TGTCTGCTCTCAAAATACAAAG 559  
RESULT 6  
AY866302 825 bp DNA linear PRI 24-JAN-2005  
LOCUS AY866302  
DEFINITION Saguinus labiatus microRNA mir-15a and microRNA mir-16-1 genes,  
complete sequence.  
ACCESSION AY866302  
VERSION AY866302.1 GI:57903104  
KEYWORDS  
SOURCE Saguinus labiatus (red-cheeked mustached tamarin)  
ORGANISM Saguinus labiatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;  
Callitrichidae; Saguinus.  
REFERENCE  
AUTHORS 1 (bases 1 to 825)  
Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H. and Cuppen,E.  
TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes

JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE 2 (bases 1 to 825)  
Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H.A. and Cuppen,E.  
AUTHORS Direct Submission  
TITLE Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht  
JOURNAL 3584 CT, The Netherlands  
LOCATION/Qualifiers  
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601..622  
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Db 448 CTTTGAGTAAAGTAGACACATATGCTTTGTGATTGAAAGGTGACGCCATAT 507  
QY 61 UGUGCUGCCUCAAUAUACAAG 83  
Db 508 TGTCTGCTCTCAAAATACAAAG 530  
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LOCUS AY866299  
DEFINITION Ateles geoffroyi microRNA mir-15a and microRNA mir-16-1 genes,  
complete sequence.  
ACCESSION AY866299  
VERSION AY866299.1 GI:57903101  
KEYWORDS  
SOURCE Ateles geoffroyi (black-handed spider monkey)  
ORGANISM Ateles geoffroyi  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;  
Cebidae; Ateleinae; Ateles.  
REFERENCE  
AUTHORS 1 (bases 1 to 836)  
Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H. and Cuppen,E.  
TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE 2 (bases 1 to 836)  
Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H.A. and Cuppen,E.  
AUTHORS Direct Submission  
TITLE Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht  
JOURNAL 3584 CT, The Netherlands  
LOCATION/Qualifiers  
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source 1..836  
/organism="Ateles geoffroyi"  
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477..498  
misc\_RNA

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QY 61 UGUGCGCCUCAAUAUACAAG 83
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Db 524 TGTGCTGCTCAAAATACAAAG 546

RESULT 8
AY866301      871 bp      DNA      linear      PRI 24-JAN-2005
LOCUS      Macaca nemestrina microRNA mir-15a and microRNA mir-16-1 genes,
DEFINITION      complete sequence.
ACCESSION      AY866301
VERSION      AY866301.1 GI:57903103
KEYWORDS
SOURCE      Macaca nemestrina (pig-tailed macaque)
ORGANISM      Macaca nemestrina
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE      1 (bases 1 to 871)
AUTHORS      Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
Plasterk,R.H., and Cuppen,E.
Phylogenetic Shadowing and Computational Identification of Human
microRNA Genes
JOURNAL      Cell 120 (1), 21-24 (2005)
PUBMED      15652478

TITLE      2 (bases 1 to 871)
AUTHORS      Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
Plasterk,R.H.A., and Cuppen,E.
Direct Submission
Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht
3584 CT, The Netherlands
FEATURES
Source      1..871
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ORIGIN
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Best Local Similarity 73.5%; Pred. No. 1.6e-20;
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

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QY 61 UGUGCGCCUCAAUAUACAAG 83
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Db 533 TGTGCTGCTCAAAATACAAAG 555
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RESULT 9
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LOCUS      Macaca mulatta microRNA mir-15a and microRNA mir-16-1 genes,
DEFINITION      complete sequence.
ACCESSION      AY866305
VERSION      AY866305.1 GI:57903107
KEYWORDS
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM      Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE      1 (bases 1 to 896)
AUTHORS      Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
Plasterk,R.H., and Cuppen,E.
Phylogenetic Shadowing and Computational Identification of Human
microRNA Genes
JOURNAL      Cell 120 (1), 21-24 (2005)
PUBMED      15652478

TITLE      2 (bases 1 to 896)
AUTHORS      Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
Plasterk,R.H.A., and Cuppen,E.
Direct Submission
Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht
3584 CT, The Netherlands
FEATURES
Source      1..896
             /organism="Macaca mulatta"
             /mol_type="genomic DNA"
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             462..544
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ORIGIN
Query Match      100.0%; Score 83; DB 5; Length 896;
Best Local Similarity 73.5%; Pred. No. 1.6e-20;
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUGAGUAAAGUAGCAGCAUAUGGCUUUGGAAUUGGAGGCGCAUAV 60
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Db 462 CCTTGAGTAAAGTAGCAGCACAATATGTTGTGGATTGTGAAAGGTGACGCAAT 521
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 UGUGCGCCUCAAUAUACAAG 83
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Db 522 TGTGCTGCTCAAAATACAAAG 544

RESULT 10
AY866300      901 bp      DNA      linear      PRI 24-JAN-2005
LOCUS      Gorilla gorilla microRNA mir-15a and microRNA mir-16-1 genes,
DEFINITION      complete sequence.
ACCESSION      AY866300
VERSION      AY866300.1 GI:57903102
KEYWORDS
SOURCE      Gorilla gorilla (gorilla)
ORGANISM      Gorilla gorilla
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Gorilla.
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REFERENCE 1 (bases 1 to 901)  
AUTHORS Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H., and Cuppen,E.  
TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE 2 (bases 1 to 901)  
AUTHORS Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H.A., and Cuppen,E.  
TITLE Direct Submission  
JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht  
3584 CT, The Netherlands  
FEATURES  
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602..690  
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Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
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Db 462 CTTTGAGTAAAGTACAGACATTAATGTTTGATTTGAAAGGTGAGCCATAT 521  
QY 61 UGUGCUGCCUCAAUAUACAAG 83  
Db 522 TGTGCTGCTCAAAAATACAAG 544  
RESULT 11  
AY866307 902 bp DNA linear PRI 24-JAN-2005  
LOCUS Pan troglodytes microRNA mir-15a and microRNA mir-16-1 genes,  
complete sequence.  
ACCESSION AY866307  
VERSION AY866307.1 GI:57903109  
KEYWORDS  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Pan.  
REFERENCE 1 (bases 1 to 902)  
AUTHORS Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H., and Cuppen,E.  
TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE 2 (bases 1 to 902)  
AUTHORS Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H.A., and Cuppen,E.  
TITLE Direct Submission  
JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht  
3584 CT, The Netherlands  
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Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
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Db 463 CTTTGAGTAAAGTACAGACATTAATGTTTGATTTGAAAGGTGAGCCCATAT 522  
QY 61 UGUGCUGCCUCAAUAUACAAG 83  
Db 523 TGTGCTGCTCAAAAATACAAG 545  
RESULT 12  
AY866303 914 bp DNA linear PRI 24-JAN-2005  
LOCUS Pan paniscus microRNA mir-15a and microRNA mir-16-1 genes, complete  
sequence.  
ACCESSION AY866303  
VERSION AY866303.1 GI:57903105  
KEYWORDS  
SOURCE Pan paniscus (pygmy chimpanzee)  
ORGANISM  
Pan paniscus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Pan.  
REFERENCE 1 (bases 1 to 914)  
AUTHORS Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H., and Cuppen,E.  
TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE 2 (bases 1 to 914)  
AUTHORS Berezikov,E., Gurjev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H.A., and Cuppen,E.  
TITLE Direct Submission  
JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalan 8, Utrecht  
3584 CT, The Netherlands  
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source  
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Oy	CCUUGAGUAAAGATGACAGACAAUAVUGUUGUUGAAAAAGGUGAGGACAAU	60
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Db	CTTTGAGTAAAGTATGACAGACATAATGTGTTTGTGATTTTGAAGAAGTGCAGGCAAT	53
	:     :     :     :     :     :     :     :     :     :	
Oy	61 UGUGCUCGCUCAAAAUAUACAAG	83
	:  :     :     :     :     :     :     :     :     :     :	
Db	535 TGTGTCCTCTTAAAAATACAAAG	557

RESULT 13					
AC069475/c					
LOCUS	AC069475	153092 bp	DNA	linear	PRI 09-APR-2003
DEFINITION	Homo sapiens chromosome 13 clone 317g11 map 13q14,			complete	

ACCESSION	AC069475	GI:11992970
VERSION	AC069475.27	
KEYWORDS	HTG.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 153092)
AUTHORS	Malaj, E., Cowell, J.K. and Roe, B.A.
TITLE	Human sapiens Chromosome 13q14 BAC clone 317g11
JOURNAL	Unpublished

REFERENCE	2 (bases 1 to 153092)
AUTHORS	Malaj, E., Cowell, J. K. and Roe, B. A.
TITLE	Direct Submission
JOURNAL	Submitted (01-JUN-2000) Department

JOURNAL  
 Submitted (01-JUN-2000) Department Of Chemistry And Biochemistry,  
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
 OK 73019, USA  
 3 (bases 1 to 153092)  
 REFERENCE  
 Authors  
 Malaj,E., Cowell,U.K. and Roe,B.A.

**JOURNAL**

REFERENCE	4 (bases 1 to 153092)
AUTHORS	Malaj, E., Cowell, J.K. and Roe, B.A.
TITLE	Direct Submission
JOURNAL	Submitted (09-APR-2003) Department-

COMMENT On Dec 27, 2000 this sequence version replaced gi:11560201.

----- genome center  
Center: Department Of Chemistry And Biochemistry  
The University Of Oklahoma  
Center code:UOKNOR

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Matches 61	Conservative	22	Mismatches 0	Indels 0
			Gaps	0

**DY**

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	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
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	:::::::::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	

**Db**

436	CCTTGGATGAAGTAGCAGCACATAATGTTCGTGANTTTGAAAAAGCGCAGCCCAT	377
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DB      376 TGTGCTGCTCAAAAATACAAGG  354

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RESULT 14	AF334404/c	LOCUS	DEFINITION	ACCSSION	VERSION
	AF334404	154868 bp	DNA linear		
	Homoc. sapiens chromosome 13q14 BAC clone C17B-369L16, complete sequence.				
	AF334404				
	AF334404.1	GI:13507269			

ORGANIC

## REFERENCE

TITLE

JOURNAL  
PUBMED  
REFERENCE

Cancer Res. 61 (7), 2870-2877 (2001)  
11306461  
2 (bases 1 to 154868)

TITLE	JOURNAL	REFERENCE
Sequencing of the chromosome 13q14 region deleted in B-CLL	Unpublished	3 (bases 1 to 154868)

**TITLE** Direct Submission  
**JOURNAL** Submitted (09-JAN-2001) Kimmel Cancer Center, Thomas Jefferson Medical College, BLSB, Rm. 1006, 233 S. 10th Street, Philadelphia, PA 19107, USA

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gene

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132819..>154868  
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gene 1 cDNA sequence presented in GenBank Accession Number  
Y15227"

Query Match	100.0%	Score 83	DB 5	Length 154868
Best Local Similarity	73.5%	Pred. No. 2.2e-20		
Matches 61	Conservative 22	Mismatches 0	Indels 0	Gaps 0

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Db 99823 CTTTGAGTAAAGTACAGCACAATATGTTTGATTTTGAAGAGTCCAGGCCATAT 99764

OY	61	UGUGCUGCCUCAA <sup>A</sup> AUA <sup>C</sup> ACAGG	83
		: : : : : : : : : : :	
Db	99763	TGTGCTGCCTCAAAATACAAGG	99741

## RESULT 15



AL137060/c  
LOCUS AL137060 154887 bp DNA linear PRI 18-MAY-2005  
DEFINITION Human DNA sequence from clone RP11-34F20 on chromosome 13 contains the 3' end of the RFP2 gene for ret finger protein 2, the DLEU2 gene for deleted in lymphocytic leukemia 2 (DLEU2 BCM5UN), the 5' end of the DLEU1 gene for deleted in lymphocytic leukemia 1 (BCM5 LEU1), a ribosomal protein L18 (RPL18) pseudogene, a novel gene and four CpG islands, complete sequence.  
ACCESSION AL137060  
VERSION AL137060.13 GI:11120982  
KEYWORDS HTG; BCM5; BCM5UN; CpG island; DLEU1; DLEU2; LEU1; LEU2; lymphocytic leukemia; RFP2; RPL18.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 154887)  
AUTHORS Pearce, A.  
TITLE Direct Submission  
JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk  
COMMENT On Nov 8, 2000 this sequence version replaced gi:11022355. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13  
RP11-34F20 is from the library RPO1-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm  
VECTOR: pBAC3.6  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: vegas@sanger.ac.uk  
-----  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.  
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BQ018724 BQ018724  
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mRNA

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gene

mRNA

gene

mRNA

gene

mRNA

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Best Local Similarity 100.0%; Score 83; DB 5; Length 154887;
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

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QY 61 UUGUGUGCCUCAAACAAUACAAG 83
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Job time : 1838.86 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 19:02:55 / Search time 397.61 Seconds  
(without alignments)  
1455.440 Million cell updates/sec

Title: US-10-706-798-1

Perfect score: 83

Sequence: 1 ccugagagaaagacagc.....gucgcucaaaaacag 83

Scoring table: IDENTITY\_NUC

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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: geneseqn2001as:\*

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6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

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14: geneseqn2005s:\*

15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	83	12	AD017089 Human miR
2	83	100.0	83	14	AEB92620 Human miR
3	83	100.0	83	14	AEB92620 Human miR
4	83	100.0	83	15	AEB92620 Human miR
5	83	100.0	83	15	AEB92620 Human miR
6	83	100.0	83	15	AEB92620 Human miR
7	83	100.0	83	15	AEB92620 Human miR
8	83	100.0	83	15	AEB92620 Human miR
9	83	100.0	83	15	AEB92620 Human miR
10	83	100.0	83	15	AEB92620 Human miR
11	83	100.0	83	15	AEB92620 Human miR
12	83	100.0	83	15	AEB92620 Human miR
13	83	100.0	83	15	AEB92620 Human miR
14	83	100.0	83	15	AEB92620 Human miR
15	83	100.0	83	15	AEB92620 Human miR
16	83	100.0	83	15	AEB92620 Human miR
17	83	100.0	83	15	AEB92620 Human miR
18	83	100.0	83	15	AEB92620 Human miR

C	19	33.4	40.2	83	15	AEB92620 Human miR
C	20	33.4	40.2	310	14	AD030808 Human miR
C	21	33.4	40.2	4214	14	Ak72317 Human miR
C	22	32.4	39.0	110	14	AD030808 Human miR
C	23	30.4	36.6	110	14	AD030808 Human miR
C	24	30.4	36.6	90001	15	AEB17143 Human miR
C	25	30.4	36.6	108	15	AEB17143 Human miR
C	26	29.6	35.7	108	14	AEB92619 Human miR
C	27	28.4	34.2	2492	4	AA61948 Human miR
C	28	28	33.7	1313	14	AEB67609 Human miR
C	29	27.6	33.3	4745	14	AEB14812 Human miR
C	30	27.4	33.0	267	8	ACA23222 Prokaryote
C	31	27.4	33.0	2843	4	AAH16588 Human CDN
C	32	27.4	33.0	4940	10	ADP82143 Leukemia
C	33	27.4	33.0	4940	10	ADP82144 Leukemia
C	34	27.4	33.0	110000	2	AAK20248 Borrelia
C	35	27.2	32.8	85	14	AD04176 Mouse pri
C	36	27.2	32.8	98	14	AEB92622 Human miR
C	37	27.2	32.8	98	15	AEB92622 Human miR
C	38	27.2	32.8	98	15	AEB92622 Human miR
C	39	27.2	32.8	110	14	AD02997 Human pri
C	40	27.2	32.8	66743	4	ABL27118 Drosophila
C	41	27	32.5	27	14	AD03789 Human pri
C	42	27	32.5	3386	13	AD047216 Bacterial
C	43	27	32.5	3396	13	AD047216 Bacterial
C	44	27	32.5	64125	13	AD033295 Human can
C	45	27	32.5	96599	10	ADC85298 Human Egr

## ALIGNMENTS

RESULT 1	AD017089	standard; RNA; 83 BP.
ID	AD017089	standard; RNA; 83 BP.
AC	AD017089;	
XX	12-AUG-2004	(first entry)
DT	12-AUG-2004	(first entry)
XX	Human miR15 precursor RNA sequence SeqID1.	
XX	miR15; miR15; cancer; proliferation; cancer cell; cytoskeletal;	
KW	gene therapy; chronic lymphocytic leukaemia; prostate cancer; micro RNA;	
KW	chromosome 13q14; human; ss.	
OS	Homo sapiens.	
FX	Key	Location/Qualifiers
FT	misc_binding	1..5
FT	misc_binding	/*tag= a
FT	misc_binding	/bound_moiety= "Binds to itself"
FT	misc_binding	/note="Forms a double stranded region with bases 83-79 of itself"
FT	misc_binding	16..23
FT	misc_binding	/*tag= b
FT	misc_binding	/bound_moiety= "Binds to itself"
FT	misc_binding	/note="Forms a double stranded region with bases 68-61 of itself"
FT	misc_binding	26..35
FT	misc_binding	/*tag= c
FT	misc_binding	/bound_moiety= "Binds to itself"
FT	misc_binding	/note="Forms a double stranded region with bases 58-49 of itself"
FT	misc_binding	38..40
FT	misc_binding	/*tag= d
FT	misc_binding	/bound_moiety= "Binds to itself"
FT	misc_binding	/note="Forms a double stranded region with bases 46-44 of itself"
FT	misc_binding	44..46
FT	misc_binding	/*tag= e
FT	misc_binding	/bound_moiety= "Binds to itself"
FT	misc_binding	/note="Forms a double stranded region with bases 40-38 of itself"

```
FT      misc_binding      of itself"
PT      49. .58
PT      /*tag= f
PT      /bound_moiety= "binds to itself"
FT      /note= "Forms a double stranded region with bases 35-26
PT      of itself"
FT      misc_binding      /*tag= g
PT      /bound_moiety= "binds to itself"
PT      /note= "Forms a double stranded region with bases 23-16
FT      of itself"
FT      misc_binding      /*tag= h
PT      /bound_moiety= "binds to itself"
PT      /note= "Forms a double stranded region with bases 5-1 of
FT      itself"
FT      WO2004043387-A2.
XX      PD
XX      27-MAY-2004.
XX      PF
XX      12-NOV-2003; 2003WO-US035777.
XX      PR
XX      13-NOV-2002; 2002US-0425864P.
XX      PR
XX      09-MAY-2003; 2003US-0469464P.
XX      PA
XX      (UYJE-) UNIV JEFFERSON THOMAS.
XX      PI
XX      Croce CM, Calin GA;
XX      WPI; 2004-400825/37.
XX      DR
XX      PT
XX      Treating an miR15 or miR16 mediated cancer, i.e. chronic lymphocytic
PT      leukemia or prostate cancer, comprises administering to the subject an
PT      miR15 or miR16 gene product.
XX      PS
XX      Claim 64; SEQ ID NO 1; 73pp; English.
XX      CC
XX      This invention relates to a novel method of treating an miR15 or miR16
CC      mediated cancer in a subject which comprises administering to the subject
CC      an amount of an isolated miR15 or miR16 gene product such that
CC      proliferation of miR15 or miR16 mediated cancer cells is inhibited. The
CC      miR15 and miR16 micro RNA genes are localised to 13q14 in humans, a
CC      region that is deleted in a significant portion of subjects suffering
CC      from chronic lymphocytic leukaemia or prostate cancer. The products of
CC      the miR15 and miR16 genes have also been found to inhibit the neoplastic
CC      or tumorigenic growth of chronic lymphocytic leukaemia or prostate
CC      cancer cells. The invention may be useful for the production of compounds
CC      with a cytostatic activity. In addition the invention may also be useful
CC      for gene therapy using the miR15 or miR16 gene product. The methods and
CC      compositions are useful in diagnosing and treating miR15 or miR16
CC      mediated cancer, i.e. chronic lymphocytic leukaemia or prostate cancer.
CC      The present sequence is that of the human miR15 precursor RNA sequence
CC      which is used in the method of the invention.
XX      SQ
XX      Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;
XX      Query Match      100.0%; Score 83; DB 12; Length 83;
XX      Best Local Similarity 100.0%; Pred. NO. 2.1e-20;
XX      Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      1 CCUUGGAGUAAAGAGACACAUAAUGGUUUUGGAAUUUUGAAAGGUGGACCAUAAU 60
XX      DB      1 CCUUGGAGUAAAGAGACACAUAAUGGUUUUGGAAUUUUGAAAGGUGGACCAUAAU 60
XX      QY      61 UGUGCUGGCTUCAAAAUAACAAG 83
XX      DB      61 UGUGCUGGCTUCAAAAUAACAAG 83
XX      RESULT 2
XX      AEB92620
XX      ID AEB92620 standard; DNA; 83 BP.
```

```
XX      AC
XX      AEB92620;
XX      DT
XX      03-NOV-2005 (first entry)
XX      DE
XX      Human microRNA gene SEQ ID NO 33.
XX      KW
XX      cyostatic; gene therapy; diagnosis; prognosis; pharmaceutical;
KW      gene expression; musculoskeletal disease; hematological disease;
KW      immunostimulant; andrology; neurological disease; dermatological disease;
KW      endocrine disease; gynecology and obstetrics; respiratory disease;
KW      gastrointestinal disease; genitourinary disease; cancer; neoplasia;
KW      microRNA; miR; ss; biochip.
XX      KW
XX      Homo sapiens.
XX      OS
XX      WO2005078139-A2.
XX      PN
XX      25-AUG-2005.
XX      PD
XX      PF
XX      09-FEB-2005; 2005WO-US004865.
XX      PR
XX      09-FEB-2004; 2004US-0542929P.
XX      PR
XX      09-FEB-2004; 2004US-0542940P.
XX      PR
XX      09-FEB-2004; 2004US-0542963P.
XX      PR
XX      09-FEB-2004; 2004US-0543119P.
XX      PR
XX      18-JUN-2004; 2004US-0580797P.
XX      PR
XX      18-JUN-2004; 2004US-0580959P.
XX      PA
XX      (UYJE-) UNIV JEFFERSON THOMAS.
XX      PI
XX      Croce CM, Liu C, Calin GA;
XX      WPI; 2005-571622/58.
XX      DR
XX      PT
XX      Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,
PT      tumors, or myelodysplastic syndrome, comprises evaluating a miR gene in
PT      the test sample.
XX      PS
XX      Example 1; SEQ ID NO 33; 170pp; English.
XX      CC
XX      The invention describes diagnosing whether a subject has, or is at risk
CC      for developing, a cancer linked to a cancer-associated chromosomal
CC      feature, comprises evaluating the status in the subject of at least one
CC      microRNA (miR) gene located in close proximity to the cancer-associated
CC      chromosomal feature. Also described are a pharmaceutical composition
CC      comprising an isolated miR gene product or a nucleic acid encoding an
CC      isolated miR gene product from an miR gene located in close proximity to
CC      a cancer-associated chromosomal feature and is not miR15 or miR16, and a
CC      pharmaceutical carrier; and a method of treating cancer associated with a
CC      cancer-associated chromosomal feature in a subject. The miR, composition,
CC      and method are useful for diagnosing and treating a cancer-associated
CC      chromosomal feature, where the cancer is bladder cancer, esophageal
CC      cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,
CC      ovarian cancer, breast cancer, lymphoma, Ewing sarcoma, hematopoietic
CC      tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,
CC      epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,
CC      head-and-neck cancer, renal cancer, male germ cell tumors, malignant
CC      mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer,
CC      prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilm's
CC      tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,
CC      neuroblastoma, leukemia (acute lymphocytic leukemia, acute myeloid
CC      leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,
CC      medulloblastoma, lymphoblastic myeloid lymphoma, rhabdomyosarcoma, B-cell
CC      chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
CC      associated with an unmutated IGHV gene, ZAP-70 expression, CD38
CC      expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or
CC      their combination. This sequence represents a human microRNA (miRNA)
CC      gene.
XX      SQ
XX      Sequence 83 BP; 26 A; 13 C; 22 G; 22 T; 0 U; 0 Other;
XX      Query Match      100.0%; Score 83; DB 14; Length 83;
```

```
Best Local Similarity 73.5%; Pred. No. 2.1e-20;
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCUGGAGUAAAGAGCAGCAUAUAGUUGUAGAUUUUGAAAGGUGCAGCCAUU 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 CTTTGAGTAAAGTAGCAGCATATAGTTTGATTTGAAAGGTGAGCCATAT 60
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 61 UGUGCUGCCUCAAUAUACAAG 83
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 TGTGCTGCTCAAAATATCAAG 83
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
AED35990
ID AED35990 standard; RNA; 83 BP.
XX
AC AED35990;
XX
DT 15-DEC-2005 (first entry)
XX
DE Human micro RNA miR-15a precursor.
XX
KM RNA interference; RNA purification; RNA amplification; gene silencing;
KW RNA detection; micro RNA; miRNA; miR-15a; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT stem_loop 1..83
FT /*tag= a
FT misc_RNA 14..35
FT /*tag= b
FT /*note= "Corresponds to mature miRNA"
XX
PN W02005098029-A2.
XX
PD 20-OCT-2005.
XX
PE 07-APR-2005; 2005WO-DK000239.
XX
PR 07-APR-2004; 2004DK-00000578.
PR 23-JUL-2004; 2004DK-00001146.
PR 11-AUG-2004; 2004DK-00001218.
PR 15-OCT-2004; 2004DK-00001587.
PR 28-JAN-2005; 2005DK-00000140.
XX
PA (EXIQ-) EXIQON AS.
XX
PI Jacobsen N, Kongsbak L, Kauppinen S, Echwald SM, Mouritzen P;
PI Nielsen PS, Norholm M;
XX
DR WPI; 2005-714540/73.
XX
PT Isolating, purifying, amplifying, detecting, identifying, quantifying or
PT capturing non-coding RNAs such as micro RNA or small interfering RNA
PT (siRNA), involves using oligonucleotide containing nucleoside analogs.
XX
PS Disclosure; Fig 29; 180pp; English.
XX
CC The present invention relates to the use of an oligonucleotide for the
CC isolation, purification, amplification, detection, identification,
CC quantification or capture of microRNA (miRNA) or small interfering RNA
CC (siRNA), where the oligonucleotide contains a number of nucleoside
CC analogs. The method uses 2 anchored tagging probes, each designed in
CC combination to detect a complementary target sequence, e.g. a short RNA
CC sequence, where the first tagging probe hybridizes to a first region
CC within a target sequence and the second tagging probe hybridizes to a
CC second region within the same complementary target sequence, e.g. a short
CC RNA target sequence that is adjacent to the first region. In a preferred
CC mode, one of the tagging probes is 5' phosphorylated to enable covalent
CC coupling of the 2 contiguous tagging probes hybridized to the
CC complementary target sequence by a ligase to form a single
CC oligonucleotide sequence. The method takes advantage of substitution of
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CC the recognition sequences with high-affinity nucleotide analogs, e.g.
CC locked nucleic acid (LNA), for sensitive and specific hybridization to
CC short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is
CC followed by real-time quantitative PCR (qPCR) of the target sequence,
CC e.g. ribonucleic acid-templated, covalently joined oligonucleotide
CC molecules using anchor sequences attached to the tagging probes as
CC priming sites for the PCR primers and a short detection probe with
CC sufficient duplex stability to allow binding to the amplicon, and
CC employing any of a variety of detection principles used in homogeneous
CC assays. In the preferred mode, the detection probe is substituted with
CC duplex-stabilizing, high-affinity nucleotide analogs, e.g. LNA, and
CC preferably oxy-LNA, to allow the use of short detection probes in the
CC real-time qPCR. The method is useful for detecting and quantifying
CC individual small RNA molecules in complex mixtures of different nucleic
CC acids, and for detecting, testing, diagnosing or quantifying miRNAs,
CC siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative mRNA
CC splice variants implicated in, or connected to, human disease in complex
CC nucleic acid samples, e.g. from cancer patients. The present sequence is
CC that of human miRNA Hsa miR-15a precursor. miR-15a AED35991 was used as
CC the target in examples from the invention.
XX
SQ Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;
XX
Query Match 100.0%; Score 83; DB 14; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCUGGAGUAAAGAGCAGCAUAUAGUUGUAGAUUUUGAAAGGUGCAGCCAUU 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 CCUGGAGUAAAGAGCAGCAUAUAGUUGUAGAUUUUGAAAGGUGCAGCCAUU 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 61 UGUGCUGCCUCAAUAUACAAG 83
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 UGUGCUGCCUCAAUAUACAAG 83
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
AEE26703
ID AEE26703 standard; RNA; 83 BP.
XX
AC AEE26703;
XX
DT 09-FEB-2006 (first entry)
XX
DE Hsa miR-15a precursor sequence, SEQ ID 72.
XX
KM RNA amplification; RNA detection; RNA purification; miRNA; microRNA; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1..5
FT /*tag= a
FT /*bound_moiety= "Nucleotides 83..79 of the present
FT sequence"
FT 13
FT /*tag= b
FT /*bound_moiety= "Nucleotide 71 of the present sequence"
FT 16..23
FT /*tag= c
FT /*bound_moiety= "Nucleotides 68..61 of the present
FT sequence"
FT 26..35
FT /*tag= d
FT /*bound_moiety= "Nucleotides 58..49 of the present
FT sequence"
FT 38..39
FT /*tag= e
FT /*bound_moiety= "Nucleotides 46..45 of the present
FT sequence"
FT 45..46
FT /*tag= f
FT /*bound_moiety= "Nucleotides 39..38 of the present
FT sequence"
```

```
FT misc_binding sequence"
FT /tag= 49. .58
FT /bound_moiety= "Nucleotides 35. .26 of the present
FT sequence"
FT misc_binding /tag= h
FT /bound_moiety= "Nucleotides 23. .16 of the present
FT sequence"
FT /tag= 71
FT /bound_moiety= "Nucleotide 13 of the present sequence"
FT misc_binding /tag= .83
FT /bound_moiety= "Nucleotides 5. .1 of the present sequence"
FT /tag= j
FT /bound_moiety= "Nucleotides 5. .1 of the present sequence"
XX US2005272075-A1.
XX
XX 08-DEC-2005.
XX
XX 07-APR-2005; 2005US-00100897.
XX
XX 07-APR-2004; 2004US-0560148P.
XX 23-JUL-2004; 2004US-0590856P.
XX 12-AUG-2004; 2004US-0600961P.
XX 15-OCT-2004; 2004US-0619291P.
XX 28-JAN-2005; 2005US-0648221P.
XX
XX (JACO/) JACOBSEN N.
XX (KONG/) KONGSBAK L.
XX (KAUP/) KAUPPINEN S.
XX (ECHW/) ECHWALD S M.
XX (MOUR/) MOURITZEN P.
XX (NIEL/) NIELSEN P S.
XX (NORH/) NORHOLM M.
XX
XX Jacobson N, Kongsbak L, Kauppinen S, Echwald SM, Mouritzen P;
XX Nielsen PS, Norholm M;
XX
XX WPI; 2006-037202/04.
XX
XX Isolating, purifying, amplifying, detecting identifying, quantifying, or
XX capturing non-coding RNAs, such as microRNA or small interfering RNA
XX (siRNA) by using an oligonucleotide containing a number of nucleoside
XX analogues.
XX
XX Disclosure: SEQ ID NO 72; 113bp; English.
XX
XX The present invention relates to novel methods for quantifying non-coding
XX RNAs, such as microRNA or short interfering RNA (siRNA). The methods
XX comprises using an oligonucleotide containing a number of nucleoside
XX analogues e.g lna analogues. The methods are useful for detecting and
XX quantifying individual small RNA molecules in complex mixtures composed
XX of hundreds of thousands of different nucleic acids. The present sequence
XX was used to illustrate the invention.
XX
XX Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;
SQ
Query Match 100.0%; Score 83; DB 15; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUAUUGGAGGUGCCCAU 60
DB 1 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUAUUGGAGGUGCCCAU 60
QY 61 UGUGCUGCCUCAAUUAUACAAG 83
DB 61 UGUGCUGCCUCAAUUAUACAAG 83
RESULT 5
AEE99350
```

```
ID AEE99350 standard; RNA; 83 BP.
XX
XX AEE99350;
AC
XX 23-FEB-2006 (first entry)
XX
XX Human miRNA sequence, hsa-mir-15a.
XX
XX RNA detection; microarray; diagnosis; genetic marker; drug screening; ss.
XX
XX Homo sapiens.
XX
XX WO2005118806-A2.
XX
XX 15-DEC-2005.
XX
XX 31-MAY-2005; 2005MO-US018826.
XX
XX 28-MAY-2004; 2004US-0575743P.
XX 03-FEB-2005; 2005US-0649584P.
XX
XX (AMBI-) AMBION INC.
XX
XX Brown D, Conrad R, Devroe E, Goldrick M, Keiger K, Labourier E;
XX Moon I, Powers P, Shelton J, Shingara J;
XX
XX WPI; 2006-047544/05.
XX
XX Multi-labeling miRNA in a sample, by forming a reaction mixture for
XX enzyme catalysis, where tailed miRNA molecules are produced, and
XX attaching a label to the tailed miRNA molecules.
XX
XX Disclosure; SEQ ID NO 22; 307bp; English.
XX
XX The new invention relates to manipulation of miRNA and their use in
XX characterizing their role and function in cells. Described is a method of
XX multi-labeling miRNA in a sample by forming a reaction mixture for enzyme
XX catalysis, comprising the miRNA with an enzyme that catalyzes the
XX addition of di- or tri-phosphate nucleotides, and one or more labeled or
XX unlabeled nucleotides, where tailed miRNA molecules are produced; and
XX attaching a label to the tailed miRNA molecules. Specifically, the method
XX comprises enriching miRNA in the sample; forming a reaction mixture,
XX under conditions that allows enzyme catalysis, where tailed miRNA
XX molecules are produced; and if unlabeled nucleotides are added to the
XX miRNA, attaching a label to the tailed miRNA molecules. Also given
XX include a miRNA array comprising one or more miRNA probes immobilized on
XX a solid support, where the probes comprise an miRNA coding sequence, and
XX an amine attached to the 5' or 3' end of the probe; evaluating miRNA in a
XX sample; identifying a correlation between miRNA expression and a disease
XX or condition; analyzing miRNA in a sample; identifying a candidate
XX diagnostic marker or therapeutic target of a disease or condition;
XX determining a difference between two or more biological samples;
XX screening for a candidate therapeutic agent for a disease or condition;
XX and a kit for preparing miRNA for multi-labeling. The methods and
XX compositions are useful for isolating, enriching, and/or labeling miRNA
XX molecule samples. The present sequence is a human miRNA sequence, used in
XX the new methods of the invention.
XX
XX Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;
SQ
Query Match 100.0%; Score 83; DB 15; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUAUUGGAGGUGCCCAU 60
DB 1 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUAUUGGAGGUGCCCAU 60
QY 61 UGUGCUGCCUCAAUUAUACAAG 83
DB 61 UGUGCUGCCUCAAUUAUACAAG 83
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PR	14-AUG-2000	2000US-02254519P
PR	14-AUG-2000	2000US-02254513P
PR	14-AUG-2000	2000US-02254514P
PR	14-AUG-2000	2000US-02254566P
PR	14-AUG-2000	2000US-02254676P
PR	14-AUG-2000	2000US-02254687P
PR	14-AUG-2000	2000US-02254688P
PR	14-AUG-2000	2000US-02254700P
PR	14-AUG-2000	2000US-02254747P
PR	14-AUG-2000	2000US-02254757P
PR	14-AUG-2000	2000US-02254758P
PR	14-AUG-2000	2000US-02254799P
PR	18-AUG-2000	2000US-02262579P
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PR	25-SEP-2000	2000US-02349978P
PR	25-SEP-2000	2000US-02354848P
PR	25-SEP-2000	2000US-02354849P
PR	26-SEP-2000	2000US-02354848P
PR	27-SEP-2000	2000US-02356344P
PR	29-SEP-2000	2000US-02358536P
PR	29-SEP-2000	2000US-02363272P
PR	29-SEP-2000	2000US-02363678P
PR	29-SEP-2000	2000US-02363688P
PR	29-SEP-2000	2000US-02363699P
PR	29-SEP-2000	2000US-02365370P
PR	02-OCT-2000	2000US-02368602P
PR	02-OCT-2000	2000US-02370378P
PR	02-OCT-2000	2000US-02370388P
PR	02-OCT-2000	2000US-02370398P
PR	02-OCT-2000	2000US-02370408P
PR	13-OCT-2000	2000US-02399355P
PR	13-OCT-2000	2000US-02409636P
PR	13-OCT-2000	2000US-02409637P
PR	20-OCT-2000	2000US-02418218P
PR	20-OCT-2000	2000US-02418258P
PR	20-OCT-2000	2000US-02418768P
PR	20-OCT-2000	2000US-02418778P
PR	20-OCT-2000	2000US-02418808P
PR	20-OCT-2000	2000US-02418898P
PR	20-OCT-2000	2000US-02418268P
PR	01-NOV-2000	2000US-02446477P
PR	08-NOV-2000	2000US-02446478P
PR	08-NOV-2000	2000US-02464758P
PR	08-NOV-2000	2000US-02464768P
PR	08-NOV-2000	2000US-02464778P
PR	08-NOV-2000	2000US-02464788P
PR	08-NOV-2000	2000US-02464798P
PR	08-NOV-2000	2000US-02464808P
PR	08-NOV-2000	2000US-02464818P
PR	08-NOV-2000	2000US-02464828P
PR	08-NOV-2000	2000US-02464838P
PR	08-NOV-2000	2000US-02464848P
PR	08-NOV-2000	2000US-02464858P
PR	08-NOV-2000	2000US-02464868P
PR	08-NOV-2000	2000US-02464878P
PR	08-NOV-2000	2000US-02464888P
PR	08-NOV-2000	2000US-02464898P
PR	08-NOV-2000	2000US-02464908P
PR	08-NOV-2000	2000US-02464918P
PR	08-NOV-2000	2000US-02464928P
PR	08-NOV-2000	2000US-02464938P
PR	08-NOV-2000	2000US-02464948P
PR	08-NOV-2000	2000US-02464958P
PR	08-NOV-2000	2000US-02464968P
PR	08-NOV-2000	2000US-02464978P
PR	08-NOV-2000	2000US-02464988P
PR	08-NOV-2000	2000US-02464998P
PR	08-NOV-200	

PR	08-NOV-2000	2000US-0246478P	
PR	08-NOV-2000	2000US-0246523P	
PR	08-NOV-2000	2000US-0246524P	
PR	08-NOV-2000	2000US-0246525P	
PR	08-NOV-2000	2000US-0246526P	
PR	08-NOV-2000	2000US-0246527P	
PR	08-NOV-2000	2000US-0246528P	
PR	08-NOV-2000	2000US-0246532P	
PR	08-NOV-2000	2000US-0246609P	
PR	08-NOV-2000	2000US-0246610P	
PR	08-NOV-2000	2000US-0246611P	
PR	08-NOV-2000	2000US-0246613P	
PR	17-NOV-2000	2000US-0249207P	
PR	17-NOV-2000	2000US-0249208P	
PR	17-NOV-2000	2000US-0249209P	
PR	17-NOV-2000	2000US-0249210P	
PR	17-NOV-2000	2000US-0249211P	
PR	17-NOV-2000	2000US-0249212P	
PR	17-NOV-2000	2000US-0249213P	
PR	17-NOV-2000	2000US-0249214P	
PR	17-NOV-2000	2000US-0249215P	
PR	17-NOV-2000	2000US-0249216P	
PR	17-NOV-2000	2000US-0249218P	
PR	17-NOV-2000	2000US-0249244P	
PR	17-NOV-2000	2000US-0249245P	
PR	17-NOV-2000	2000US-0249264P	
PR	17-NOV-2000	2000US-0249265P	
PR	17-NOV-2000	2000US-0249297P	
PR	17-NOV-2000	2000US-0249299P	
PR	17-NOV-2000	2000US-0249300P	
PR	01-DEC-2000	2000US-0250160P	
PR	01-DEC-2000	2000US-0250391P	
PR	05-DEC-2000	2000US-0251030P	
PR	05-DEC-2000	2000US-0251988P	
PR	05-DEC-2000	2000US-0256719P	
PR	06-DEC-2000	2000US-0251479P	
PR	08-DEC-2000	2000US-0251856P	
PR	08-DEC-2000	2000US-0251868P	
PR	08-DEC-2000	2000US-0251869P	
PR	08-DEC-2000	2000US-0251989P	
PR	11-DEC-2000	2000US-0251990P	
PR	11-DEC-2000	2000US-0254097P	
PR	05-JAN-2001	2001US-0253678P	
PA	(HUMA-) HUMAN GENOME SCI INC.		
PI	Rosen CA, Barash SC, Ruben SM;		
PI	WPI; 2001-483426/52.		
PT	Nucleic acids encoding human immune/haematopoietic antigen polypeptides,		
PT	useful for preventing, diagnosing and/or treating cancers and metastasis.		
XX	Disclosure; SEQ ID NO 27129; 3071bp + Sequence Listing; English.		
XX	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)		
XX	amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic		
XX	activity, and can be used in gene therapy and vaccine production. (I)		
XX	proteins and polynucleotides may be used in the prevention, diagnosis and		
XX	treatment of diseases associated with inappropriate (I) expression. For		
XX	expression, they may be used to treat disorders associated with decreased		
XX	expression by rectifying mutations or deletions in a patient's genome		
XX	that affect the activity of (I) by expressing inactive proteins or to		
XX	supplement the patient's own production of (I). Additionally, (I)		
XX	polynucleotides may be used to produce the secreted (I), by inserting the		
XX	nucleic acids into a host cell and culturing the cell to express the		
XX	protein. (I) proteins and polynucleotides may be used to prevent,		
XX	diagnose and treat immune/haematopoietic-related diseases, especially		
XX	cancers and cancer metastases of haematopoietic-derived cells. AAK64703		
XX	to AAK87694 represent human immune/haematopoietic antigen genomic		
XX	sequences from the present invention. AAK51942 to AAK54950 and AAM82169		
XX	represent sequences used in the exemplification of the present invention		



```
XX Sequence 4214 BP; 1348 A; 698 C; 794 G; 1374 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 83; DB 4; Length 4214;
Best Local Similarity 73.5%; Pred. No. 7,8e-20;
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUGAGUAAAGUAGACGACACAUAAUGGUTUGAUAUUUGAAAAGUGCAGGCCCAUUAU 60
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB CTTTGAGTAAGTAAAGACGACGACATATGTTGTGATTTTGAAGAGTGACAGCCATAT 2875
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 61 UGUGCUGCCUCAAUUAUACAAG 83
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 2876 TGTGCTGCTCCTCAAAATAACAAG 2898
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 8
ADXX03045
ID ADXX03045 standard; RNA; 110 BP.
XX
AC ADXX03045;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human primary microRNA (pri-miRNA) mir-15a-1.
XX
XX MicroRNA; de; RNA interference; gene silencing; Cytostatic; Antidiabetic;
XX Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive;
XX Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
XX Bating-Disorder-Gen.; hyperproliferation; cancer; neoplasm;
XX angiogenesis disorder; cardiovascular disease;
XX non-insulin dependent diabetes; endocrine disease;
XX gastrointestinal disease; metabolic disorder; obesity;
XX nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
XX hypertension; anorexia nervosa; nutritional disorder;
XX psychiatric disorder; Alzheimer's disease; degeneration;
XX neurological disease; nervous system injury; neurodegenerative disease;
XX neurological disorder.
XX
XX Homo sapiens.
XX
XX WO2005013901-A2.
XX
XX 17-FEB-2005.
XX
XX 30-JUL-2004; 2004WO-US025300.
XX
XX 31-JUL-2003; 2003US-0492056P.
XX 31-OCT-2003; 2003US-0516303P.
XX 19-DEC-2003; 2003US-0531596P.
XX 14-APR-2004; 2004US-0562417P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF,
XX Vickers T, Marcuseon EG, Koller E, Swayze EE, Jain R, Bhat B,
XX Peralta E;
XX
XX WPI; 2005-163123/17.
XX
XX New oligomeric compound that can hybridize with or sterically interfere
XX with nucleic acid molecules comprising or encoding small non-coding RNA
XX targets, useful for treating e.g., cancer and diabetes.
XX
XX Example 3; SEQ ID NO 128; 854pp; English.
XX
XX The invention relates to an oligomeric compound comprising a first region
XX and a second region, where at least one region contains a modification,
XX and a portion of the oligomeric compound is targeted to a small non-
XX coding RNA target nucleic acid that is miRNA (micro-RNA), or its
XX precursor (primary-miRNA, pri-miRNA). Also included are a composition
XX comprising a first oligomeric compound and a second oligomeric compound
XX (where at least one of the oligomeric compounds contains a modification,
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```
CC at least a portion of the first oligomeric compound is capable of
CC hybridizing with at least a portion of the second oligomeric compound,
CC and at least a portion of the first oligomeric compound is targeted to a
CC small non-coding RNA target nucleic acid), a pharmaceutical composition
CC comprising the composition cited above (and a carrier), a kit or assay
CC device comprising the composition, modulating the expression of a small
CC non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC treating or preventing a disease or disorder associated with a small non-
CC coding RNA target nucleic acid, treating a condition in an animal,
CC treating or preventing a disease or disorder associated with CD36,
CC methods of screening an oligomeric compound for an effect on miRNA
CC signaling, methods of screening a miRNA precursor for an effect in miRNA
CC signaling, methods of modulating translation (or apoptosis, conversion of
CC a precursor miRNA into miRNA, or cellular differentiation), identifying
CC an RNA transcript bound to a small non-coding RNA, arresting (or
CC delaying) entry of a cell at the G2/M phase, interfering with chromosome
CC segregation, a method of triggering apoptosis, detecting a miRNA
CC precursor, identifying a miRNA target, modulating cellular
CC differentiation, treating a condition associated with adipocyte
CC differentiation in an animal, treating/preventing a disease/disorder
CC associated with aberrant regulation of the cell cycle by miRNAs,
CC maintaining a pluripotent stem cell and identifying a small non-coding
CC RNA binding site. The oligomeric compound is targeted to a region
CC flanking a Drosha cleavage site within a pri-miRNA. It stimulates an
CC increase in expression of a pri-miRNA. The compounds and compositions are
CC useful for treating a disease or disorder resulting from chromosomal non-
CC disjunction, altered methylation, acetylation, or pseudouridylation state
CC of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia,
CC Alzheimer's disease, a central nervous system injury or neurodegenerative
CC disorder. The present sequence is a primary miRNA of the invention.
XX
SQ Sequence 110 BP; 40 A; 15 C; 26 G; 0 T; 29 U; 0 Other;
Query Match 98.8%; Score 82; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.3e-20;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUGAGUAAAGUAGACGACACAUAAUGGUTUGAUAUUUGAAAAGUGCAGGCCCAUUAU 60
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 29 CCUUGAGUAAAGUAGACGACACAUAAUGGUTUGAUAUUUGAAAAGUGCAGGCCCAUUAU 88
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 61 UGUGCUGCCUCAAUUAUACAAG 82
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 89 UGUGCUGCCUCAAUUAUACAAG 110
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 9
ADXX03080
ID ADXX03080 standard; RNA; 110 BP.
XX
AC ADXX03080;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human primary microRNA (pri-miRNA) mir-15a-2.
XX
XX MicroRNA; de; RNA interference; gene silencing; Cytostatic; Antidiabetic;
XX Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive;
XX Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
XX Bating-Disorder-Gen.; hyperproliferation; cancer; neoplasm;
XX angiogenesis disorder; cardiovascular disease;
XX non-insulin dependent diabetes; endocrine disease;
XX gastrointestinal disease; metabolic disorder; obesity;
XX nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
XX hypertension; anorexia nervosa; nutritional disorder;
XX psychiatric disorder; Alzheimer's disease; degeneration;
XX neurological disease; nervous system injury; neurodegenerative disease;
XX neurological disorder.
XX
XX Homo sapiens.
XX
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PN WO2005013901-A2.  
XX 17-FEB-2005.  
XX 30-JUL-2004; 2004WO-US025300.  
XX 31-JUL-2003; 2003US-0492056P.  
PR 31-OCT-2003; 2003US-0516303P.  
PR 19-DEC-2003; 2003US-0531596P.  
PR 14-APR-2004; 2004US-0562417P.  
XX (ISIS-) ISIS PHARM INC.  
XX Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF,  
P1 Vickers T, Marcusson EG, Koller E, Swayze EE, Jain R, Bhat B;  
P1 Peralta E;  
XX WPI; 2005-163123/17.  
XX New oligomeric compound that can hybridize with or sterically interfere  
PT with nucleic acid molecules comprising or encoding small non-coding RNA  
PT targets, useful for treating e.g., cancer and diabetes.  
XX Example 3; SEQ ID NO 165; 854pp; English.  
XX The invention relates to an oligomeric compound comprising a first region  
XX and a second region, where at least one region contains a modification,  
XX and a portion of the oligomeric compound is targeted to a small non-  
XX coding RNA target nucleic acid that is miRNA (micro-RNA), or its  
XX precursor (primary-miRNA, pri-miRNA). Also included are a composition  
XX comprising a first oligomeric compound and a second oligomeric compound  
XX (where at least one of the oligomeric compounds contains a modification,  
XX at least a portion of the first oligomeric compound is capable of  
XX hybridizing with at least a portion of the second oligomeric compound,  
XX and at least a portion of the first oligomeric compound is targeted to a  
XX small non-coding RNA target nucleic acid), a pharmaceutical composition  
XX comprising the composition cited above (and a carrier), a kit or assay  
XX device comprising the composition, modulating the expression of a small  
XX non-coding RNA target nucleic acid in a cell (or tissue or animal),  
XX treating or preventing a disease or disorder associated with a small non-  
XX coding RNA target nucleic acid, treating a condition in an animal,  
XX treating or preventing a disease or disorder associated with C936,  
XX methods of screening an oligomeric compound for an effect on miRNA  
XX signaling, methods of screening a miRNA precursor for an effect in miRNA  
XX signaling, methods of modulating translation (or apoptosis, conversion of  
XX a precursor miRNA into miRNA, or cellular differentiation), identifying  
XX an RNA transcript bound to a small non-coding RNA, arresting (or  
XX delaying) entry of a cell at the G2/M phase, interfering with chromosome  
XX segregation, a method of triggering apoptosis, detecting a miRNA  
XX precursor, identifying a miRNA target, modulating cellular  
XX differentiation, treating a condition associated with adipocyte  
XX differentiation in an animal, treating/preventing a disease/disorder  
XX associated with aberrant regulation of the cell cycle by miRNAs,  
XX maintaining a pluripotent stem cell and identifying a small non-coding  
XX RNA binding site. The oligomeric compound is targeted to a region  
XX flanking a Droscha cleavage site within a pri-miRNA. It stimulates an  
XX increase in expression of a pri-miRNA. The compounds and compositions are  
XX useful for treating a disease or disorder resulting from chromosomal non-  
XX distinction, altered methylation, acetylation, or pseudouridylation state  
XX of chromosomes, such as a hyperproliferative condition (e.g. cancer,  
XX neoplasia or angiosgenesis), diabetes (Type 2 diabetes), obesity,  
XX hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia,  
XX Alzheimer's disease, a central nervous system injury or neurodegenerative  
XX disorder. The present sequence is a primary miRNA of the invention.  
XX  
SQ Sequence 110 BP; 39 A; 15 C; 27 G; 0 T; 29 U; 0 Other;  
Query Match 96.4%; Score 80; DB 14; Length 110;  
Best Local Similarity 100.0%; Pred. No. 2.9e-19;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCUTGAGUAAAGUGACGACACAUANUGGUTUUGGAAUUGGUGAGGCCCAU 60  
|||||

Db 31 CCUTGAGUAAAGUGACGACACAUANUGGUTUUGGAAUUGGUGAGGCCCAU 90  
QY 61 UGUGCTUGCCUCAAUAAUACA 80  
|||  
Db 91 UGUGCTUGCCUCAAUAAUACA 110  
|||  
RESULT 10  
ID AEB92619 standard; DNA; 108 BP.  
XX AEB92619;  
AC AEB92619;  
XX  
DT 03-NOV-2005 (first entry)  
XX  
DE Human microRNA gene SEQ ID NO 32.  
XX  
KW cyrostatic; gene therapy; diagnosis; prognosis; pharmaceutical;  
KW gene expression; musculoskeletal disease; hematological disease;  
KW immunostimulant; andrology; neurological disease; dermatological disease;  
KW endocrine disease; gynecology and obstetrics; respiratory disease;  
KW gastrointestinal disease; genitourinary disease; cancer; neoplasm;  
KW microRNA; miR; ss; biochip.  
XX  
XX Homo sapiens.  
XX  
XX WO2005078139-A2.  
XX  
XX 25-AUG-2005.  
XX  
XX 09-FEB-2005; 2005NO-US004865.  
XX  
XX 09-FEB-2004; 2004US-0542929P.  
XX  
XX 09-FEB-2004; 2004US-0542929P.  
XX  
XX 09-FEB-2004; 2004US-0542940P.  
XX  
XX 09-FEB-2004; 2004US-0542963P.  
XX  
XX 09-FEB-2004; 2004US-0543119P.  
XX  
XX 18-JUN-2004; 2004US-0580797P.  
XX  
XX 18-JUN-2004; 2004US-0580959P.  
XX  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
XX Croce CM, Liu C, Calin GA;  
XX  
XX WPI; 2005-571622/58.  
XX  
XX Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,  
PT tumor, or myelodysplastic syndrome, comprises evaluating a miR gene in  
PT the test sample.  
XX  
XX Example 1; SEQ ID NO 32; 170pp; English.  
XX  
XX The invention describes diagnosing whether a subject has, or is at risk  
XX for developing, a cancer linked to a cancer-associated chromosomal  
XX feature, comprises evaluating the status in the subject of at least one  
XX microRNA (miR) gene located in close proximity to the cancer-associated  
XX chromosomal feature. Also described are a pharmaceutical composition  
XX comprising an isolated miR gene product or a nucleic acid encoding an  
XX isolated miR gene product from an miR gene located in close proximity to  
XX a cancer-associated chromosomal feature and is not miR15 or miR16, and a  
XX pharmaceutical carrier, and a method of treating cancer associated with a  
XX cancer-associated chromosomal feature in a subject. The miR, composition,  
XX and method are useful for diagnosing and treating a cancer-associated  
XX chromosomal feature, where the cancer is bladder cancer, cervical cancer,  
XX cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,  
XX ovarian cancer, breast cancer, lymphoma, Ewing sarcoma, hematopoietic  
XX tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,  
XX epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,  
XX head-and-neck cancer, renal cancer, male germ cell tumors, malignant  
XX mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer,  
XX prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilm's  
XX tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,  
XX neuroblastoma, leukemia (acute lymphocytic leukemia, acute myeloid  
XX leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,



```
XX The invention relates to an oligomeric compound comprising a first region
CC and a second region, where at least one region contains a modification,
CC and a portion of the oligomeric compound is targeted to a small non-
CC coding RNA target nucleic acid that is miRNA (micro-RNA) or its
CC precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC comprising a first oligomeric compound and a second oligomeric compound
CC (where at least one of the oligomeric compounds contains a modification,
CC at least a portion of the first oligomeric compound is capable of
CC hybridizing with at least a portion of the second oligomeric compound,
CC and at least a portion of the first oligomeric compound is targeted to a
CC small non-coding RNA target nucleic acid), a pharmaceutical composition
CC comprising the composition cited above (and a carrier, a kit or assay
CC device comprising the composition, modulating the expression of a small
CC non-coding RNA target nucleic acid in a cell (or tissue or animal)),
CC treating or preventing a disease or disorder associated with a small non-
CC coding RNA target nucleic acid, treating a condition in an animal,
CC treating or preventing a disease or disorder associated with CD36,
CC methods of screening an oligomeric compound for an effect on miRNA
CC signaling, methods of screening a miRNA precursor for an effect in miRNA
CC signaling, methods of modulating translation (or apoptosis, conversion of
CC a precursor miRNA into miRNA, or cellular differentiation), identifying
CC an RNA transcript bound to a small non-coding RNA, arresting (or
CC delaying) entry of a cell at the G2/M phase, interfering with chromosome
CC segregation, a method of triggering apoptosis, detecting a miRNA
CC precursor, identifying a miRNA target, modulating cellular
CC differentiation, treating a condition associated with adipocyte
CC differentiation in an animal, treating/preventing a disease/disorder
CC associated with aberrant regulation of the cell cycle by miRNAs,
CC maintaining a pluripotent stem cell and identifying a small non-coding
CC RNA binding site. The oligomeric compound is targeted to a region
CC flanking a Drosophila cleavage site within a pri-miRNA. It stimulates an
CC increase in expression of a pri-miRNA. The compounds and compositions are
CC useful for treating a disease or disorder resulting from chromosomal non-
CC disjunction, altered methylation, acetylation, or pseudouridylation state
CC of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia,
CC Alzheimer's disease, a central nervous system injury or neurodegenerative
CC disorder. The present sequence is a primary miRNA of the invention.
XX
SQ Sequence 70 BP; 23 A; 12 C; 18 G; 0 T; 17 U; 0 Other;
Query Match 74.5%; Score 61.8; DB 14; Length 70;
Best Local Similarity 96.9%; Pred. No. 1.2e-12;
Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 11 AAGUAGCGCACUAUUGGUGGUAUUGGAAAGGUGCAGGCCAUAUUGUGUGCCU 70
DB 1 AAGUAGCGCACUAUUGGUGGUAUUGGAAAGGUGCAGGCCAUAUUGUGUGCCU 60
OY 71 CAAAA 75
DB 61 CAAAA 65
RESULT 13
ID AEB92912 standard; DNA; 40 BP.
AC AEB92912;
XX
DT 03-NOV-2005 (first entry)
XX
DE Human microRNA gene probe SEQ ID NO 325.
XX
KW cytosstatic; gene therapy; diagnosis; prognosis; pharmaceutical;
KW gene expression; musculoskeletal disease; hematological disease;
KW immunostimulant; andrology; neurological disease; dermatological disease;
KW endocrine disease; gynecology and obstetrics; respiratory disease;
KW gastrointestinal disease; genitourinary disease; cancer; neoplasm;
KW microRNA; miR; ss; biocchip; probe.
XX
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OS Homo sapiens.
PN WO2005078139-A2.
XX
PD 25-AUG-2005.
XX
PF 09-FEB-2005; 2005WO-US004865.
XX
PR 09-FEB-2004; 2004US-0542929P.
PR 09-FEB-2004; 2004US-0542940P.
PR 09-FEB-2004; 2004US-0542963P.
PR 09-FEB-2004; 2004US-0543119P.
PR 18-JUN-2004; 2004US-0580797P.
PR 18-JUN-2004; 2004US-0580959P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Croce CM, Liu C, Calin GA;
XX
DR WPI; 2005-571622/58.
XX
PT Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,
PT tumors, or myelodysplastic syndrome, comprises evaluating a miR gene in
PT the test sample.
XX
PS Example 10; SEQ ID NO 325, 170pp; English.
XX
SQ The invention describes diagnosing whether a subject has, or is at risk
CC for developing, a cancer linked to a cancer-associated chromosomal
CC feature, comprises evaluating the status in the subject of at least one
CC chromosomal feature. Also described are a pharmaceutical composition
CC comprising an isolated miR gene product or a nucleic acid encoding an
CC isolated miR gene product from an miR gene located in close proximity to
CC a cancer-associated chromosomal feature and is not miR15 or miR16, and a
CC pharmaceutical carrier, and a method of treating cancer associated with a
CC cancer-associated chromosomal feature in a subject. The miR, composition,
CC and method are useful for diagnosing and treating a cancer-associated
CC chromosomal feature, where the cancer is bladder cancer, esophageal
CC cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,
CC ovarian cancer, breast cancer, lymphoma, Ewing sarcoma, hematopoietic
CC tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,
CC epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,
CC head-and-neck cancer, renal cancer, male germ cell tumors, malignant
CC mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer,
CC prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilms'
CC tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,
CC neuroblastoma, leukemia (acute lymphocytic leukemia, acute myeloid
CC leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,
CC medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell
CC chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
CC associated with an unmutated IgVH gene, ZAP-70 expression, CD38
CC expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or
CC their combination. This sequence represents a human microRNA (miRNA) gene
CC probe used in the creation of an oligonucleotide microchip for miRNA
CC profiling.
XX
SQ Sequence 40 BP; 11 A; 5 C; 11 G; 13 T; 0 U; 0 Other;
Query Match 48.2%; Score 40; DB 14; Length 40;
Best Local Similarity 67.5%; Pred. No. 0.00011;
Matches 27; Conservative 13; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCUUGAGUAAAGUAGCAGCAUAUUGGUGGUAUUG 40
DB 1 CCTTGAGTAAGTAGCAGCACTAATGCTTTGGCATTT 40
RESULT 14
ID AEB92913 standard; DNA; 40 BP.
XX
AC AEB92913;
```

XX	03-NOV-2005	(first entry)	
DT			
DE	Human microRNA gene probe SEQ ID NO 326.		
XX			
XX			
KW	cytosolic; gene therapy; diagnosis; prognosis; pharmaceutical;		
KW	gene expression; musculoskeletal disease; hematological disease;		
KW	immunostimulant; andrology; neurological disease; dermatological disease;		
KW	endocrine disease; gynecology and obstetrics; respiratory disease;		
KW	gastrointestinal disease; genitourinary disease; cancer; neoplasm;		
XX	microRNA; miR; ss; biochip; probe.		
OS			
CS	Homo sapiens.		
XX			
PN	WO2005078139-A2.		
PD			
XX	25-AUG-2005.		
PF			
XX	09-FEB-2005; 2005WO-US004865.		
XX			
XX	09-FEB-2004; 2004US-0542929P.		
PR	09-FEB-2004; 2004US-0542940P.		
PR	09-FEB-2004; 2004US-0542963P.		
PR	09-FEB-2004; 2004US-054119P.		
PR	18-JUN-2004; 2004US-0580797P.		
PR	18-JUN-2004; 2004US-0580959P.		
XX			
PA	(UYJE-) UNIV JEFFERSON THOMAS.		
PI			
FI	Croce CM, Liu C, Calin GA;		
DR	WPI; 2005-571622/58.		
XX			
PT	Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,		
PT	tumors, or myelodysplastic syndrome, comprises evaluating a miR gene in		
PT	the test sample.		
XX			
PS	Example 10; SEQ ID NO 326; 170bp; English.		
XX			
CC	The invention describes diagnosing whether a subject has, or is at risk		
CC	for developing, a cancer linked to a cancer-associated chromosomal		
CC	feature, comprises evaluating the status in the subject of at least one		
CC	microRNA (miR) gene located in close proximity to the cancer-associated		
CC	chromosomal feature. Also described are a pharmaceutical composition		
CC	comprising an isolated miR gene product or a nucleic acid encoding an		
CC	isolated miR gene product from an miR gene located in close proximity to		
CC	a cancer-associated chromosomal feature and is not miR15 or miR16, and a		
CC	pharmaceutical carrier; and a method of treating cancer associated with a		
CC	cancer-associated chromosomal feature in a subject. The miR, composition,		
CC	and method are useful for diagnosing and treating a cancer-associated		
CC	chromosomal feature, where the cancer is bladder cancer, esophageal		
CC	cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,		
CC	ovarian cancer, breast cancer, lymphoma, Ewing sarcoma, hematopoietic		
CC	tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,		
CC	epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,		
CC	head-and-neck cancer, renal cancer, male germ cell tumors, malignant		
CC	mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer,		
CC	prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilms		
CC	tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,		
CC	neuroblastoma, leukemia (acute lymphocytic leukemia, acute myeloid		
CC	leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,		
CC	medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell		
CC	chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia		
CC	associated with an unmutated IgH gene, ZAP-70 expression, CD38		
CC	expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or		
CC	their combination. This sequence represents a human microRNA (miRNA) gene		
CC	probe used in the creation of an oligonucleotide microchip for miRNA		
CC	profiling.		
XX			
XX	Sequence 40 BF; 6 A; 6 C; 12 G; 14 T; 0 U; 0 Other;		
XX			
Query Match	48.2%;	Score 40;	DB 14; Length 40;
Best Local Similarity	65.0%;	Pred No. 0.00011;	

[illegible]



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 20:21:19 ; Search time 3848.83 Seconds  
(without alignments)  
1205.901 Million cell updates/sec

Title: US-10-706-798-1

Perfect score: 83  
1 ccuugaggaagaaagacagc.....gcugccuacaaauacaag 83

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est3: \*  
3: gb\_est4: \*  
4: gb\_est5: \*  
5: gb\_est6: \*  
6: gb\_est7: \*  
7: gb\_est8: \*  
8: gb\_est9: \*  
9: gb\_est10: \*  
10: gb\_est11: \*  
11: gb\_est12: \*  
12: gb\_est13: \*  
13: gb\_est14: \*  
14: gb\_est15: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	77.2	93.0	486	11	A0672199 HS_2151_B
C 2	71.8	86.5	638	11	A2938498 2M0197A08
C 3	36.8	44.3	330	14	DR22A19S
C 4	34.4	41.4	893	14	CNS032XX
C 5	32.4	39.0	486	11	A0672199
C 6	31	37.3	348	10	DR975958
C 7	30.6	36.9	690	11	A2830728
C 8	30.4	36.6	409	8	CV259755
C 9	30.4	36.6	669	11	A2955179
C 10	30.4	36.6	826	5	CK791915
C 11	30	36.1	657	12	CE734321
C 12	30	36.1	901	14	CT224114
C 13	29.8	35.9	752	8	CK206707
C 14	29.2	35.2	832	7	BE538951
C 15	29	34.9	266	1	AL701112
C 16	29	34.9	617	4	CH503344
C 17	28.8	34.7	557	7	BE228377
C 18	28.8	34.7	797	9	CK492605
C 19	28.8	34.7	820	9	CK405012

C 20	28.8	34.7	822	11	B2117274	B2117274
C 21	28.6	34.5	541	9	DA287889	DA287889
C 22	28.6	34.5	765	14	CT385120	CT385120
C 23	28.6	34.5	793	12	CC925298	CC925298
C 24	28.4	34.2	445	12	CE142086	CE142086
C 25	28.4	34.2	633	13	CM371850	CM371850
C 26	28.4	34.2	786	9	CK829205	CK829205
C 27	28.4	34.2	1019	12	CL039913	CL039913
C 28	28.2	34.0	538	8	CO159141	CO159141
C 29	28.2	34.0	551	11	B2148619	B2148619
C 30	28.2	34.0	554	11	A0693353	A0693353
C 31	28.2	34.0	664	5	CP387823	CP387823
C 32	28.2	34.0	691	5	CP387852	CP387852
C 33	28.2	34.0	719	8	CO366636	CO366636
C 34	28.2	34.0	829	11	B2205743	B2205743
C 35	28.2	34.0	835	9	DN462069	DN462069
C 36	28.2	34.0	906	13	CL992915	CL992915
C 37	28.2	34.0	908	10	DT626902	DT626902
C 38	28.2	34.0	917	13	CZ792260	CZ792260
C 39	28	33.7	433	5	CK058325	CK058325
C 40	28	33.7	446	1	AU173105	AU173105
C 41	28	33.7	466	5	CK048847	CK048847
C 42	28	33.7	516	5	CK035528	CK035528
C 43	28	33.7	536	5	CK083202	CK083202
C 44	28	33.7	543	14	CNS005WP	AL088951
C 45	28	33.7	549	9	CK632947	CK632947

#### ALIGNMENTS

RESULT 1  
A0672199/c  
LOCUS  
DEFINITION  
A0672199 486 bp DNA linear GSS 24-JUN-1999  
HS\_2151\_B1\_B12\_MR CIT Approved Human Genomic Sperm Library D Homo  
sapiens genomic clone Plate=2151 Col=23 Row=D, genomic survey  
sequence.

ACCESSION  
A0672199  
VERSION  
A0672199.1 GI:5204870  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 486)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.

TITLE  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
PUBMED  
10449764  
COMMENT  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: http://www.htsc.washington.edu  
Plate: 2151 row: D column: 23  
Seq primer: M13 Reverse  
Class: BAC ends  
High quality sequence stop: 486.  
Location/Qualifiers  
1. 486

FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=2151 Col=23 Row=D"  
/sex="male"





sequence.  
ACCESSION AL225438  
VERSION AL225438.1 GI:788433  
KEYWORDS GSS: genome survey sequence.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1  
AUTHORS Roest Croollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizeser,C., Winkler,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
PUBMED 10835645

REFERENCE 2  
AUTHORS Roest Croollius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C., Fizeser,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Genome Res. 10 (7), 939-949 (2000)  
PUBMED 10899143

REFERENCE 3 (bases 1 to 893)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
COMMENT - Web : www.genoscope.cns.fr  
This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.  
FEATURES  
source  
1..893  
/organism="Tetraodon nigroviridis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:99883"  
/clone\_1fb="207L24"  
/clone\_1lb="G"  
/note="Genoscope sequence ID : COAG207DF12LP1 end : 17"

ORIGIN  
Query Match 41.4%; Score 34.4; DB 14; Length 893;  
Best Local Similarity 51.7%; Pred. No. 1.3;  
Matches 31; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 13 GUACGACGACUAAUGUUGUUGAUAAGGUGCCGACGUAUUGUGUGCCGCA 72  
Db 630 GTACGACGACGAAAGGTTGTGAGTTACCTGAGATTCAGGCAATGCTGTCGCGCA 689

RESULT 5  
LOCUS AO672199 486 bp DNA linear GSS 24-JUN-1999  
DEFINITION HS\_2151\_B12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2151 Col=23 Row=D, genomic survey sequence.  
ACCESSION AO672199  
VERSION AO672199  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo  
1 (bases 1 to 486)  
Mahaitas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Kellar,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
COMMENT Contact: Mahaitas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: http://www.htsc.washington.edu  
Plate: 2151 row: D column: 23  
Seq primer: M13 Reverse  
Class: BAC ends  
High quality sequence stop: 486.  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=2151 Col=23 Row=D"  
/sex="male"  
/clone\_1fb="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

ORIGIN  
Query Match 39.0%; Score 32.4; DB 11; Length 486;  
Best Local Similarity 44.6%; Pred. No. 5.7;  
Matches 37; Conservative 14; Mismatches 32; Indels 0; Gaps 0;

Qy 1 CCUGGAGUAAAGAGGACGACAUUAGUUGUUGAUAAGGUGCCGCAUAV 60  
Db 358 CCTGTGATTTCTTGAGGACGACATATGAGCTGACCTTTCAAAATACAAACATTA 417

Qy 61 UGUGCUGCCUCUCAAUAUACAAG 83  
Db 418 TGTCCTGCTACTTATCTNCAAG 440

RESULT 6  
LOCUS DR975958/c 348 bp mRNA linear EST 03-JAN-2006  
DEFINITION Skin-13\_B03\_PDR-LTB-SF11A A. transmontanus skin express library  
ACCESSION DR975958  
VERSION DR975958.1 GI:84178869  
KEYWORDS EST.  
SOURCE Acipenser transmontanus (white sturgeon)  
ORGANISM Acipenser transmontanus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae; Acipenser.  
1 (bases 1 to 348)  
Mariani,V., Malinverni,R. and Giuffrè,E.  
Transcriptome analysis of the American sturgeon (Acipenser transmontanus): pathways of gene expression in the spleen and skin unpublished (2005)  
JOURNAL Contact: Valentina Mariani  
Livesstock Genomics 1  
PMP-CERSA  
Via Einstein, Loc. Ca.na Codazza, 26900 Lodi (LO), Italy  
Email: valentina.mariani@tecnoparco.org.  
Location/Qualifiers  
1..348  
/organism="Acipenser transmontanus"  
/mol\_type="mRNA"  
/db\_xref="taxon:7904"  
/clone\_1fb="A. transmontanus skin express library"  
/note="Organ: skin"



ORIGIN

Qy	62	GUGCUGCCUCAAUAUCAA	81	
	: . :	:		
Db	28	GTGGTGAATCAAAAAAAAAA	9	

ACCESSION	AZ955179
VERSION	AZ955179.1
KEYWORDS	GI:13826406
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 669)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
Unpublished (2000)  
Contact: Robert B. Weiss  
COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA

Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0221 row: K column: 10  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence. stop: 669.

**FEATURES**

**SOURCE**

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2M0221K1.0"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC2M library"
/notes="Vector: PMW427; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
laboratory Mouse DNA Resource

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**ORIGIN**

Query Match	36.6%;	Score	30.4;	DB	11;	Length	669;
Best Local Similarity	43.8%;	Pred.	No. 29;				
Matches	28;	Conservative	15;	Mismatches	21;	Indels	0;
						Gaps	0;

QY 11 AAGNAGCAGCACAUAAUGUUUUGUGAUUUUGAAAGAUGCGACGCCAUUAUUGUCUGCCU 70  
Db 562 AAGNAGCTGAAACAATTAGTTTAAAGSTTTTAAAATAGATATGCATATTTTTCCTTT 621

Qy	71	CAAA	74
Db	622	CAAA	625

RESULT 10	CK791915	826 bp	mRNA	linear	EST 25-FEB-2004
LOCUS	CK791915				
DEFINITION	ABENECOURT 1860624 NIH_MGC_230	mus	musculus	cDNA clone	
IMAGE:30646441	5', mRNA sequence.				

ACCESSION	CK/91915	GI:428039111
VERSION	CK791915.1	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

ORGANISM      Mus musculus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 826)

REFERENCE	1 (bases 1 to 826)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard, Ph.D.

National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: Shicko Kimura/Atsushi Yamada, (NCI, CCR)  
cDNA Library Preparation: Express Genomics  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: NDM1149 row: i column: 10  
High quality sequence step: 643.

**FEATURES**

**SOURCE**

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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30846441"
/tissue_type="Pooled thymoids from 5 mice"
/lab_host="Dm10B Tona"
/clone_1b="NH_MGC_230"
note="Organ: thymoid; Vector: pExpress-1; Site_1: Nci1
Site_2: Nci1; RNA obtained from 5 normal wild-type mice"

```

thyroid. cDNA was primed using oligo-dT primer:  
5'-pGACTAGTCTGATCGGAGCGCCGCTT-25-3' and cloned into  
the EcoRV/NorI sites of pEXpress-1. Size-selection 1.4 kb  
resulted in an average insert size of 1.2 kb. Normalized  
version of this library is NIH\_MGC\_19191 library constructed  
by Express Genomics (Frederick, MD). Note: this is a  
NIH\_MGC Library."

## ORIGIN

Query Match 36.6%; Score 30.4; DB 5; Length 826;

Best Local Similarity 47.2%; Pred. No. 30;

Matches 34; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 7 AGUAAAGUAGCACAUAUUGUUUGAUUUUGAAAGUCAGGCCAUUUGUCU 66  
DB 570 AATATATTAACTATGATGATGGTGAAGACCTTGAAGAGTGAGGCTTAACCTTGAT 629  
QY 67 GCCUCAAAAUUA 78  
DB 630 CCTGCATTAATA 641

## RESULT 11

CE734321/c 657 bp DNA linear GSS 30-SEP-2003  
LOCUS tigr-gss-dog-17000330179737 Dog library Canis familiaris genomic,  
DEFINITION genomic survey sequence.

ACCESSION CE734321  
VERSION CE734321.1 GI:37074441  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 657)  
AUTHORS Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1998-1903 (2003)  
COMMENT 14512627

CONTACT: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.  
Location/Qualifiers

FEATURES  
source 1..657  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: Batxi; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 36.1%; Score 30; DB 12; Length 657;

Best Local Similarity 42.9%; Pred. No. 40;

Matches 30; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 12 AGUAGCAGCACAUAUUGUUUGAUUUUGAAAGUCAGGCCAUUUGUCUCCU 71  
DB 564 AGTAAAGGCAATCTCTGCTTGAACACTTGAACAGGACGACTTTTGTGCTT 505  
QY 72 AAAAAUCAA 81  
DB 504 CAGACTAGAA 495

RESULT 12  
CT224114/c 901 bp DNA linear GSS 02-NOV-2005  
LOCUS CT224114  
DEFINITION Sus scrofa genomic clone CH242-234B11, genomic survey sequence.  
ACCESSION CT224114  
VERSION CT224114.1 GI:79766278  
KEYWORDS GSS.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 901)  
AUTHORS Humphray,S.J., Plumb,R.W. and Durham,J.L.  
TITLE Direct Submission  
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Unpublished  
This sequence was generated from the SP6 end of BAC 234B11. 234B11  
is part of the CHORI-242 BAC library created by P. de Jong. Further  
details: [http://www.sanger.ac.uk/Projects/S\\_scrofa/](http://www.sanger.ac.uk/Projects/S_scrofa/).

## COMMENT

Location/Qualifiers

FEATURES  
source 1..901  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9823"  
/clone="CH242-234B11"  
/tissue\_type="White blood cells"  
/note="vector pTRABAC1.3\_BamHI  
sex female"

## ORIGIN

Query Match 36.1%; Score 30; DB 14; Length 901;

Best Local Similarity 48.6%; Pred. No. 42;

Matches 34; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 11 AAGUAGCAGCACAUAUUGUUUGAUUUUGAAAGUCAGGCCAUUUGUCUCCU 70  
DB 480 AACTAACAGCATTAAGAGGCTTGAGAAATCTTATGTCACCAAAATATTAAAGACT 421  
QY 71 CAAAAATACA 80  
DB 420 CAAACATACA 411

## RESULT 13

LOCUS CX206707 752 bp mRNA linear EST 29-DEC-2004  
DEFINITION MNS11072 Mouse Neurosphere Normalized cDNA library Mus musculus  
ACCESSION CX206707  
VERSION CX206707.1 GI:56861999  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 752)  
AUTHORS Williams,C., Wirta,V., Lundberg,J. and Friesen,J.  
TITLE Expressed sequence tags of cDNA clones from murine neurospheres  
JOURNAL Unpublished (2005)  
COMMENT Contact: Williams, C.  
Molecular Biotechnology  
Institution of Biotechnology  
Albano University Center, KTH-Royal Institute of Technology, 106  
91 Stockholm, Sweden  
Tel: +4685378332.  
Fax: +4685378481.  
Email: cecilia.williams@biotech.kth.se  
Seq primer: M13RW  
Location/Qualifiers

## FEATURES



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GENERAL INFORMATION:  
APPLICANT: Allen, Steve  
TITLE OF INVENTION: STARCH RI PHOSPHORYLATION PROTEINS  
FILE REFERENCE: B01158 US CIP  
CURRENT FILING DATE: 2000-11-15  
PRIORITY FILING DATE: 2000-11-15  
PRIORITY FILING DATE: 1998-04-09  
PRIORITY FILING DATE: 1999-04-08  
PRIORITY FILING DATE: 1999-04-08  
PRIORITY FILING DATE: 2000-10-05  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 19  
LENGTH: 4745  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-713-273A-19

Query Match 33.3%; Score 27.6; DB 3; Length 4745;  
Best Local Similarity 45.9%; Pred. No. 3.1;  
Matches 34; Conservative 11; Mismatches 29; Indels 0; Gaps 0;

OY 3 UUGAGUUAAGUAGCAGCACAUAUUGUUUGAUUUUGAAAGUGCAGGCCCAUAUUG 62  
DB 1706 TTGGTGGGAAGAGCAGAGAGAGATTTGGCAATGGCAAGGTACAGCCAGTTCT 1765

OY 63 UGUGCCUCUAAAA 76  
DB 1766 TGTGAATAAATA 1779

RESULT 3  
US-09-949-016-11945  
Sequence 11945, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C0001307  
CURRENT FILING DATE: 2000-04-14  
CURRENT FILING DATE: 2000-04-14  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY FILING DATE: 2000-10-03  
PRIORITY FILING DATE: 2000-09-08  
PRIORITY FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11945  
LENGTH: 86439  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-11945

Query Match 33.0%; Score 27.4; DB 3; Length 86439;  
Best Local Similarity 43.5%; Pred. No. 11;  
Matches 30; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

OY 9 UAAAGUACAGCACAUAUUGUUUGAUUUUGAAAGUGCAGGCCCAUAUUGUGCUC 68  
DB 49398 TACAGCAGATCTGAACCTGAATCTGGCTTCTGAACATGGCATTCCATGTGTTCTCA 49457

OY 69 CUCAAAAAT 77  
DB 49458 TTCAAAATT 49466

RESULT 4

US-09-949-016-16990  
Sequence 16990, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C0001307  
CURRENT FILING DATE: 2000-04-14  
CURRENT FILING DATE: 2000-04-14  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY FILING DATE: 2000-10-03  
PRIORITY FILING DATE: 2000-10-03  
PRIORITY FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16990  
LENGTH: 86440  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16990

Query Match 33.0%; Score 27.4; DB 3; Length 86440;  
Best Local Similarity 43.5%; Pred. No. 11;  
Matches 30; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

OY 9 UAAAGUACAGCACAUAUUGUUUGAUUUUGAAAGUGCAGGCCCAUAUUGCUC 68  
DB 49398 TACAGCAGATCTGAACCTGAATCTGGCTTCTGAACATGGCATTCCATGTGTTCTCA 49457

OY 69 CUCAAAAAT 77  
DB 49458 TTCAAAATT 49466

RESULT 5  
US-09-949-016-15584  
Sequence 15584, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C0001307  
CURRENT FILING DATE: 2000-04-14  
CURRENT FILING DATE: 2000-04-14  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY FILING DATE: 2000-10-20  
PRIORITY FILING DATE: 2000-10-03  
PRIORITY FILING DATE: 2000-09-08  
PRIORITY FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15584  
LENGTH: 194915  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(194915)  
OTHER INFORMATION: n = A, T, C or G  
US-09-949-016-15584

Query Match 33.0%; Score 27.4; DB 3; Length 194915;  
Best Local Similarity 41.6%; Pred. No. 15;  
Matches 32; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

OY 3 UUGAGUUAAGUAGCAGCACAUAUUGUUUGAUUUUGAAAGUGCAGGCCCAUAUUG 62  
DB 5285 TTAGATTAAGATTAATTAAGCATTAATAATTAATTTGACTATTTGGAGGAGCAAACTTTTG 5344



QY 63 UGCGCCUCAAUAUAC 79  
Db 5345 AGCTGCCTCACTATCC 5361

## RESULT 6

US-09-614-221A-280  
; Sequence 280, Application US/09614221A  
; Patent No. 6723837  
; GENERAL INFORMATION:  
; APPLICANT: Karunanandaa, Balasubramanian  
; APPLICANT: Yu, Jaehyuk  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED  
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM  
; FILE REFERENCE: 16516 075  
; CURRENT APPLICATION NUMBER: US/09/614,221A  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/142,981  
; NUMBER OF SEQ ID NOS: 626  
; SEQ ID NO 280  
; LENGTH: 3396  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-09-614-221A-280

Query Match 32.5%; Score 27; DB 3; Length 3396;  
Best Local Similarity 40.3%; Pred. No. 4.6;  
Matches 27; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 13 GUACGACGACAUAAUGUUGAUUUUGAAAGUGCAGCCAUUUUGUGCCUCA 72  
Db 2173 GTCACAAAATAATGTAATGATTTGAAATACCTGACAAAGTTCTTATGCTTCAACA 2232

QY 73 AAAAUAC 79  
Db 2233 GATGTAC 2239

## RESULT 7

US-09-487-558B-71  
; Sequence 71, Application US/09487558B  
; Patent No. 6949356  
; GENERAL INFORMATION:  
; APPLICANT: Busby, Robert  
; APPLICANT: Call, Brian  
; APPLICANT: Hecht, Peter  
; APPLICANT: Holtzman, Doug  
; APPLICANT: Madden, Kevin  
; APPLICANT: Maxon, Mary  
; APPLICANT: Milne, Todd  
; APPLICANT: No. 6949356man, Thea  
; APPLICANT: Royer, John  
; APPLICANT: Salama, Sofie  
; APPLICANT: Sherman, Amir  
; APPLICANT: Silva, Jeff  
; APPLICANT: Summers, Eric  
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
; FILE REFERENCE: 109272.130  
; CURRENT APPLICATION NUMBER: US/09/487,558B  
; PRIOR FILING DATE: 2000-01-19  
; PRIOR APPLICATION NUMBER: US 60/487,558  
; NUMBER OF SEQ ID NOS: 446  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 71  
; LENGTH: 3396  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-09-487-558B-71

Query Match 32.5%; Score 27; DB 3; Length 3396;  
Best Local Similarity 40.3%; Pred. No. 4.6;  
Matches 27; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 13 GUACGACGACAUAAUGUUGAUUUUGAAAGUGCAGCCAUUUUGUGCCUCA 72  
Db 2173 GTCACAAAATAATGTAATGATTTGAAATACCTGACAAAGTTCTTATGCTTCAACA 2232

QY 73 AAAAUAC 79  
Db 2233 GATGTAC 2239

## RESULT 8

US-09-949-002-814  
; Sequence 814, Application US/09949002  
; Patent No. 6900016  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/231,401  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 814  
; LENGTH: 13614  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(13614)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-002-814

Query Match 32.3%; Score 26.8; DB 3; Length 13614;  
Best Local Similarity 44.3%; Pred. No. 9.1;  
Matches 31; Conservative 12; Mismatches 27; Indels 0; Gaps 0;

QY 2 CUUGAGUAAAGUACGACAUAAUGUUGAUUUUGAAAGUGCAGCCAUUUUG 61  
Db 3261 CTTGACAGACTGATGTAATTAATGAATGGATTAATAAGAGGGCTGCCCTTGT 3320

QY 62 UGCGCCUAC 71  
Db 3321 GTTTTGCC 3330

## RESULT 9

US-09-287-648-3922  
; Sequence 3922, Application US/09297648  
; Patent No. 6964868  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Lewis T.  
; APPLICANT: Escobedo, Jaime  
; APPLICANT: Innis, Michael A.  
; APPLICANT: Garcia, Pablo Dominguez  
; APPLICANT: Sudduth-Klinger, Julie  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Gleese, Klaus  
; APPLICANT: Randazzo, Filippo  
; APPLICANT: Kennedy, Giulia C.  
; APPLICANT: Pot, David  
; APPLICANT: Kaasan, Altaf  
; APPLICANT: Lamson, George  
; APPLICANT: Drmanac, Radoje  
; APPLICANT: Crikvenjakov, Radomir  
; APPLICANT: Dickson, Mark  
; APPLICANT: Drmanac, Snezana

APPLICANT: Labat, Ivan  
APPLICANT: Leshkowitz, Dena  
APPLICANT: Kita, David  
APPLICANT: Garcia, Veronica  
APPLICANT: Jones, William Lee  
APPLICANT: Stache-Crain, Birjic  
TITLE OF INVENTION: No. 6964868e1 Human Genes and Gene Expression  
FILE REFERENCE: 2300-1481  
CURRENT APPLICATION NUMBER: US/09/297,648  
CURRENT FILING DATE: 2000-03-10  
PRIOR APPLICATION NUMBER: 60/072,910  
PRIOR FILING DATE: 1998-01-28  
PRIOR APPLICATION NUMBER: 60/075,954  
PRIOR FILING DATE: 1998-02-24  
PRIOR APPLICATION NUMBER: 60/080,666  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: 60/080,515  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: 60/080,114  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/105,214  
PRIOR FILING DATE: 1998-10-21  
NUMBER OF SEQ ID NOS: 5252  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3922  
LENGTH: 745  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(745)  
OTHER INFORMATION: n = A,T,C or G  
US-09-297-648-1922

Query Match 31.8%; Score 26.4; DB 4; Length 745;  
Best Local Similarity 47.5%; Pred. No. 4.4;  
Matches 29; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy 21 ACAUAGUGUUGGAGUUGGAGGCGCAUUGUGCGCCUCAAUUAUACA 80  
Db 495 ACATATGTGACTGTTTTCGACAGTGCACAGCCACATTCGATGCTTGAAGAGAGA 554

Qy 81 A 81  
Db 555 A 555

RESULT 10  
US-08-669-408B-9/c  
Sequence 9, Application US/08669408B  
Patent No. 6100055  
GENERAL INFORMATION:  
APPLICANT: GUS, Bengt  
APPLICANT: JONSSON, Hans  
APPLICANT: LINDBERG, Martin  
APPLICANT: MUELLER, Hans-Peter  
APPLICANT: RANTAMAKI, Liisa K.  
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,408B  
FILING DATE: 03-JUL-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/SE94/00826  
FILING DATE: 06-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9302855-3  
FILING DATE: 06-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 61743/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1555 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 288..1526  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 288..1526  
US-08-669-408B-9

Query Match 31.8%; Score 26.4; DB 3; Length 1555;  
Best Local Similarity 35.5%; Pred. No. 5.8;  
Matches 27; Conservative 18; Mismatches 31; Indels 0; Gaps 0;

Qy 2 CUGGAGUUAAGUGGACGACACAUAGUUGUUGAGUUGAGGCGCCAUU 61  
Db 891 CTTTAGTGTAGTGTGCTTAAAGCTTTTCTGTTAAACGTCGTCATCTTATTT 832

Qy 62 GUGGCGCCUCAAU 77  
Db 831 GAGATTTCTCAAAAT 816

RESULT 11  
US-09-949-016-13209  
Sequence 13209, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13209  
LENGTH: 198942  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(198942)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13209

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Query Match      31.8%; Score 26.4; DB 3; Length 198942;
Best Local Similarity 45.0%; Pred. No. 35;
Matches 27; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy      3 UUGAGUAAGUACAGCAGCAUAUUGUUGUUGAUAAGGUCGAGCCAUUUG 62
Db      141503 TTGTGTGACCCACGACGAGAAATGGCTTTGCAATTTAAAGGGGAAAGAAAGATG 141562

RESULT 12
US-09-949-016--50534/C
; Sequence 50534, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50534
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-50534

Query Match      31.3%; Score 26; DB 3; Length 601;
Best Local Similarity 43.3%; Pred. No. 5.8;
Matches 26; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

Qy      3 UUGAGUAAGUACAGCAGCAUAUUGUUGUUGAUAAGGUCGAGCCAUUUG 62
Db      345 TTGTGTGACCCACGACGAGAAATGGCTTTGCAATTTAAAGGGGAAAGAAAGATG 286

RESULT 13
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6503729
; FILE REFERENCE: jannaschi1
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschi1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84773)..(84773)
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OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (98343)..(98343)
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; NAME/KEY: misc_feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (559241)..(559241)
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? OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Query Match          31.1%; Score 25.8; DB 3; Length 1664976;
Best Local Similarity 39.3%; Pred. No. 1.2e+02;
Matches 24; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

OY      22  CAUAAAGCUTUUGGAGUUNUTUGAAAGUGCAGGCCAUNATUGUGCGGCCUCAAUAAAADUCAA 81
Db       842845  CAAATAAGTACTGATTCGATTTTCATCACTTGACGCCCTTATTGTCCAACTAAGTCGTCAA 842904

OY      82  G  82
Db       842905  G  842905

RESULT 14
US-09-692-570-1
? Sequence 1, Application US/09692570
? Patent No. 6797466
? GENERAL INFORMATION:
? APPLICANT: Bult et al.
? TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
? Patent No. 6797466
? TITLE OF INVENTION: jannaschii
? FILE REFERENCE: PB275C1
? CURRENT APPLICATION NUMBER: US/09/692,570
? CURRENT FILING DATE: 2003-01-14
? PRIOR APPLICATION NUMBER: US 60/024,428
? PRIOR FILING DATE: 1996-08-22
? PRIOR APPLICATION NUMBER: US 08/916,421
? PRIOR FILING DATE: 1997-08-22
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 1
? LENGTH: 1664976
? TYPE: DNA
? ORGANISM: Methanococcus jannaschii
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (28222)..(28222)
? OTHER INFORMATION: n equals a, t, c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (28257)..(28258)
? OTHER INFORMATION: n equals a, t, c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (84773)..(84773)
? OTHER INFORMATION: n equals a, t, c, or g
? FEATURE:
? NAME/KEY: misc_feature
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? OTHER INFORMATION: n equals a, t, c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (84812)..(84812)
? OTHER INFORMATION: n equals a, t, c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (98120)..(98120)
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? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (98159)..(98159)
? OTHER INFORMATION: n equals a, t, c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (98239)..(98239)
? OTHER INFORMATION: n equals a, t, c, or g
? FEATURE:
? NAME/KEY: misc_feature

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LOCATION: (98266)..(98266)  
OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
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OTHER INFORMATION: n equals a, t, c, or g  
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OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
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LOCATION: (312837)..(312837)  
OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
LOCATION: (312993)..(312993)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (559167)..(559167)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (559241)..(559241)  
OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
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NAME/KEY: misc\_feature  
LOCATION: (622708)..(622708)  
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NAME/KEY: misc\_feature  
LOCATION: (657081)..(657081)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (674435)..(674435)  
OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
LOCATION: (682442)..(682442)  
OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
LOCATION: (713652)..(713652)  
OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
LOCATION: (741684)..(741684)  
OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
LOCATION: (779455)..(779455)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (779676)..(779676)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (855539)..(855539)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (871619)..(871619)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1084830)..(1084830)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1096846)..(1096846)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1119881)..(1119881)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1130881)..(1130881)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1313224)..(1313224)  
OTHER INFORMATION: n equals a, t, c, or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1349473)..(1349473)  
OTHER INFORMATION: n equals a, t, c, or g

Query Match 31.1%; Score 25.8; DB 3; Length 1664976;  
 Best Local Similarity 39.3%; Pred. No. 1.2e+02;  
 Matches 24; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 22 CAUAAUGUUUGAUAUUUGAAAAGUGCAGGCCAUUAUUGUCCUCAAUUAUACA 81  
 DB 842845 CATATAGTACTGATTTTCTTCACTTGACGCCCTTATTGTCCCACTAAGTCGTCAA 842904

QY 82 G 82  
 DB 842905 G 842905

RESULT 15

US-09-949-016-30704  
 ; Sequence 30704, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: C1001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 30704  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-30704

Query Match 30.8%; Score 25.6; DB 3; Length 601;  
 Best Local Similarity 52.1%; Pred. No. 8.2; Mismatches 14; Indels 0; Gaps 0;  
 Matches 25; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 11 AAGUAGCAGCACAUAUUGUUUGAUAUUUGAAAAGUGCAGGCCAU 58  
 DB 203 AAGAAACAGCTCATTCATTCGAAATGTTTGAAGATGACGCTCTT 250

Search completed: November 1, 2006, 22:24:29  
 Job time : 154.867 secs



Publication No. US20050059005A1  
GENERAL INFORMATION:  
APPLICANT: Tuschl, Thomas  
APPLICANT: Lagos-Quintana, Mariana  
APPLICANT: Lendeckel, Winfried  
APPLICANT: Meyer, Jutta  
APPLICANT: Rahhut, Reinhard  
TITLE OF INVENTION: MicroRNA Molecules  
FILE REFERENCE: 2923-613  
CURRENT APPLICATION NUMBER: US/10/490,955  
CURRENT FILING DATE: 2004-03-29  
PRIOR APPLICATION NUMBER: PCT/EP02/10881  
PRIOR FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: EP 02 016 772.2  
PRIOR FILING DATE: 2002-07-26  
PRIOR APPLICATION NUMBER: EP 02 006 712.0  
PRIOR FILING DATE: 2002-03-22  
PRIOR APPLICATION NUMBER: EP 01 123 453.1  
PRIOR FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 562  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 248  
LENGTH: 83  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-490-955-248

Query Match 100.0%; Score 83; DB 10; Length 83;  
Best Local Similarity 100.0%; Pred. No. 3,3e-19;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAGUAAAGUAGCAGCAUAUGUUUGUAGUUUUAAGGUGCAGGCCCAU 60  
DB 1 CCUGAGUAAAGUAGCAGCAUAUAUGUUUGUAGUUUUAAGGUGCAGGCCCAU 60  
QY 61 UGUGUCGUCUCAAUAUACAAG 83  
DB 61 UGUGUCGUCUCAAUAUACAAG 83

## RESULT 3

US-10-490-955-305  
Sequence 305, Application US/10490955  
Publication No. US20050059005A1  
GENERAL INFORMATION:  
APPLICANT: Tuschl, Thomas  
APPLICANT: Lagos-Quintana, Mariana  
APPLICANT: Lendeckel, Winfried  
APPLICANT: Meyer, Jutta  
APPLICANT: Rahhut, Reinhard  
TITLE OF INVENTION: MicroRNA Molecules  
FILE REFERENCE: 2923-613  
CURRENT APPLICATION NUMBER: US/10/490,955  
CURRENT FILING DATE: 2004-03-29  
PRIOR APPLICATION NUMBER: PCT/EP02/10881  
PRIOR FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: EP 02 016 772.2  
PRIOR FILING DATE: 2002-07-26  
PRIOR APPLICATION NUMBER: EP 02 006 712.0  
PRIOR FILING DATE: 2002-03-22  
PRIOR APPLICATION NUMBER: EP 01 123 453.1  
PRIOR FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 562  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 305  
LENGTH: 83  
TYPE: RNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: D. melanogaster or H. sapiens or M. musculus or C. elegans or  
US-10-490-955-305

Query Match 100.0%; Score 83; DB 10; Length 83;  
Best Local Similarity 100.0%; Pred. No. 3,3e-19;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAGUAAAGUAGCAGCAUAUGUUUGUAGUUUUAAGGUGCAGGCCCAU 60  
DB 1 CCUGAGUAAAGUAGCAGCAUAUAUGUUUGUAGUUUUAAGGUGCAGGCCCAU 60  
QY 61 UGUGUCGUCUCAAUAUACAAG 83  
DB 61 UGUGUCGUCUCAAUAUACAAG 83

## RESULT 4

US-11-100-897-72  
Sequence 72, Application US/11100897  
Publication No. US20050272075A1  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, Nana  
APPLICANT: Kongsbak, Lars  
APPLICANT: Kauppinen, Sakari  
APPLICANT: Echwald, Soren Mogenshaler  
APPLICANT: Mouritzen, Peter  
APPLICANT: Nielsen, Peter Stein  
APPLICANT: Nethoim, Mikkel  
TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF MICRORNAs AND SMALL  
FILE REFERENCE: 50287/013004  
CURRENT APPLICATION NUMBER: US/11/100,897  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/648,221  
PRIOR FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: 60/619,291  
PRIOR FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: 60/600,961  
PRIOR FILING DATE: 2004-08-12  
PRIOR APPLICATION NUMBER: 60/590,856  
PRIOR FILING DATE: 2004-07-23  
PRIOR APPLICATION NUMBER: 60/560,148  
PRIOR FILING DATE: 2004-04-07  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 72  
LENGTH: 83  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-100-897-72

Query Match 100.0%; Score 83; DB 15; Length 83;  
Best Local Similarity 100.0%; Pred. No. 3,3e-19;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAGUAAAGUAGCAGCAUAUGUUUGUAGUUUUAAGGUGCAGGCCCAU 60  
DB 1 CCUGAGUAAAGUAGCAGCAUAUAUGUUUGUAGUUUUAAGGUGCAGGCCCAU 60  
QY 61 UGUGUCGUCUCAAUAUACAAG 83  
DB 61 UGUGUCGUCUCAAUAUACAAG 83

## RESULT 5

US-11-230-992-1  
Sequence 1, Application US/11230992  
Publication No. US20060073505A1  
GENERAL INFORMATION:  
APPLICANT: Richard H. Griffey  
APPLICANT: Ravi Jain  
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS EFFECTING  
TITLE OF INVENTION: DROSHA-MEDIATED CLEAVAGE  
FILE REFERENCE: CORE0041US  
CURRENT APPLICATION NUMBER: US/11/230,992  
CURRENT FILING DATE: 2005-09-20



;; PRIOR APPLICATION NUMBER: 60/612,059  
;; PRIOR FILING DATE: 2004-09-21  
;; NUMBER OF SEQ ID NOS: 54  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 83  
;; TYPE: RNA  
;; ORGANISM: H. Sapiens  
US-10-909-125-906

Query Match 100.0%; Score 83; DB 16; Length 83;  
Best Local Similarity 100.0%; Pred. No. 3.3e-19;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUUUUGAAAAGGUGCAGGCCCAUAV 60  
|||  
DB 1 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUUUUGAAAAGGUGCAGGCCCAUAV 60  
|||  
QY 61 UGUGCUGCCUCAAUAUACAAG 83  
|||  
DB 61 UGUGCUGCCUCAAUAUACAAG 83  
|||

RESULT 6  
US-10-909-125-906  
; Sequence 906, Application US/10909125  
; Publication No. US20050261218A1  
; GENERAL INFORMATION:  
; APPLICANT: Esau, Christine  
; APPLICANT: Lollio, Bridget  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Freiler, Susan M.  
; APPLICANT: Griffey, Richard H.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: Vickers, Timothy  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Koller, Erich  
; APPLICANT: Swayze, Eric  
; APPLICANT: Jain, Ravi  
; APPLICANT: Bhat, Balkrishen  
; APPLICANT: Peralta, Bigen  
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation  
; TITLE OF INVENTION: Of Small Non-Coding RNAs  
; FILE REFERENCE: ISIS0080-100 (CORE0016US)  
; CURRENT APPLICATION NUMBER: US/10/909,125  
; CURRENT FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: US 60/492,056  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: US 60/516,303  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: US 60/531,596  
; PRIOR FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: US 60/562,417  
; PRIOR FILING DATE: 2004-04-14  
; NUMBER OF SEQ ID NOS: 2184  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 906  
; LENGTH: 310  
; TYPE: DNA  
; ORGANISM: H. sapien  
US-10-909-125-906

Query Match 100.0%; Score 83; DB 10; Length 310;  
Best Local Similarity 73.5%; Pred. No. 5.1e-19;  
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUUUUGAAAAGGUGCAGGCCCAUAV 60  
|||  
DB 131 CCTTGAGTAAAGTAGCAGCACATATGTTTGAGATTTGAAAAGGTGACGCCCATAT 190  
|||  
QY 61 UGUGCUGCCUCAAUAUACAAG 83  
|||  
DB 191 TGTGCTGCTCAAAATATACAAG 213  
|||

RESULT 7  
US-10-909-125-128  
; Sequence 128, Application US/10909125  
; Publication No. US20050261218A1  
; GENERAL INFORMATION:  
; APPLICANT: Esau, Christine  
; APPLICANT: Lollio, Bridget  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Freiler, Susan M.  
; APPLICANT: Griffey, Richard H.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: Vickers, Timothy  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Koller, Erich  
; APPLICANT: Swayze, Eric  
; APPLICANT: Jain, Ravi  
; APPLICANT: Bhat, Balkrishen  
; APPLICANT: Peralta, Bigen  
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation  
; TITLE OF INVENTION: Of Small Non-Coding RNAs  
; FILE REFERENCE: ISIS0080-100 (CORE0016US)  
; CURRENT APPLICATION NUMBER: US/10/909,125  
; CURRENT FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: US 60/492,056  
; PRIOR FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: US 60/516,303  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: US 60/531,596  
; PRIOR FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: US 60/562,417  
; PRIOR FILING DATE: 2004-04-14  
; NUMBER OF SEQ ID NOS: 2184  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 128  
; LENGTH: 110  
; TYPE: RNA  
; ORGANISM: H. sapiens  
US-10-909-125-128

Query Match 98.8%; Score 82; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 8.3e-19;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUUUUGAAAAGGUGCAGGCCCAUAV 60  
|||  
DB 29 CCUUGAGUAAAGUAGCACAUAUAGUUUGUGAUUUUGAAAAGGUGCAGGCCCAUAV 88  
|||  
QY 61 UGUGCUGCCUCAAUAUACAAG 82  
|||  
DB 89 UGUGCUGCCUCAAUAUACAAG 110  
|||

RESULT 8  
US-10-909-125-165  
; Sequence 165, Application US/10909125  
; Publication No. US20050261218A1  
; GENERAL INFORMATION:  
; APPLICANT: Esau, Christine  
; APPLICANT: Lollio, Bridget  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Freiler, Susan M.  
; APPLICANT: Griffey, Richard H.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: Vickers, Timothy  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Koller, Erich  
; APPLICANT: Swayze, Eric  
; APPLICANT: Jain, Ravi  
; APPLICANT: Bhat, Balkrishen  
; APPLICANT: Peralta, Bigen  
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation

TITLE OF INVENTION: Of Small Non-Coding RNAs  
FILE REFERENCE: ISIS0080-100 (CORE00160S)  
CURRENT APPLICATION NUMBER: US/10/909,125  
CURRENT FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: US 60/492,056  
PRIOR FILING DATE: 2003-07-31  
PRIOR APPLICATION NUMBER: US 60/516,303  
PRIOR FILING DATE: 2003-10-31  
PRIOR APPLICATION NUMBER: US 60/531,596  
PRIOR FILING DATE: 2003-12-19  
PRIOR APPLICATION NUMBER: US 60/562,417  
PRIOR FILING DATE: 2004-04-14  
NUMBER OF SEQ ID NOS: 2184  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 165  
LENGTH: 110  
TYPE: RNA  
ORGANISM: H. sapiens  
US-10-909-125-165

Query Match 96.4%; Score 80; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 4.3e-18; Indels 0; Gaps 0;  
Matches 80; Conservative 0; Mismatches 0;

Oy 1 CCUUGAGUAAAGUAGCAGCAUUAUGUUUGUAGAUUUUGAAAAGUGCAGGCCAUU 60  
Db 31 CCUUGAGUAAAGUAGCAGCAUUAUGUUUGUAGAUUUUGAAAAGUGCAGGCCAUU 90

Oy 61 UGUGCGCCUCAAUAUACA 80  
Db 91 UGUGCGCCUCAAUAUACA 110

RESULT 9  
US-10-909-125-1316

Sequence 1316, Application US/10909125  
Publication No. US20050261218A1  
GENERAL INFORMATION:

APPLICANT: Beau, Christine  
APPLICANT: Lollio, Bridget  
APPLICANT: Bennett, C. Frank  
APPLICANT: Freier, Susan M.  
APPLICANT: Griffee, Richard H.  
APPLICANT: Baker, Brenda F.  
APPLICANT: Vickers, Timothy  
APPLICANT: Marcusson, Eric G.  
APPLICANT: Koller, Erich  
APPLICANT: Swayze, Eric  
APPLICANT: Jain, Ravi  
APPLICANT: Bhat, Balkrishen  
APPLICANT: Peralta, Bigen  
TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation  
FILE REFERENCE: ISIS0080-100 (CORE00160S)  
CURRENT APPLICATION NUMBER: US/10/909,125  
CURRENT FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: US 60/492,056  
PRIOR FILING DATE: 2003-07-31  
PRIOR APPLICATION NUMBER: US 60/516,303  
PRIOR FILING DATE: 2003-10-31  
PRIOR APPLICATION NUMBER: US 60/531,596  
PRIOR FILING DATE: 2003-12-19  
PRIOR APPLICATION NUMBER: US 60/562,417  
PRIOR FILING DATE: 2004-04-14  
NUMBER OF SEQ ID NOS: 2184  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1316  
LENGTH: 70  
TYPE: RNA  
ORGANISM: Mouse  
US-10-909-125-1316

Query Match 74.5%; Score 61.8; DB 10; Length 70;

Best Local Similarity 96.9%; Pred. No. 1.1e-11;  
Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 11 AAGUAGCAGCAUUAUGUUUGUAGAUUUUGAAAAGUGCAGGCCAUUUGUGUGCCU 70  
Db 1 AAGUAGCAGCAUUAUGUUUGUAGAUUUUGAAAAGUGCAGGCCAUUUGUGUGCCU 60

Oy 71 CAAA 75  
Db 61 CAAA 65

RESULT 10  
US-10-706-798-1/c

Sequence 1, Application US/10706798  
Publication No. US20040152112A1  
GENERAL INFORMATION:

APPLICANT: Croce, Carlo M.  
APPLICANT: Callin, George A.  
TITLE OF INVENTION: Compositions and Methods for Cancer  
FILE REFERENCE: 08321-0126US1  
CURRENT APPLICATION NUMBER: US/10/706,798

CURRENT FILING DATE: 2003-11-12  
PRIOR APPLICATION NUMBER: 60/425,864  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: 60/469,464  
PRIOR FILING DATE: 2003-05-09

NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1  
LENGTH: 83  
TYPE: RNA

ORGANISM: Homo sapiens  
US-10-706-798-1

Query Match 40.2%; Score 33.4; DB 8; Length 83;  
Best Local Similarity 45.8%; Pred. No. 0.15; Indels 31; Gaps 0;  
Matches 38; Conservative 14; Mismatches 31;

Oy 1 CCUUGAGUAAAGUAGCAGCAUUAUGUUUGUAGAUUUUGAAAAGUGCAGGCCAUU 60  
Db 83 CCUGTAATTTTGGAGCAGCAATATGCGCTGACCTTTCAAAATCCCAACATTA 24

Oy 61 UGUGCGCCUCAAUAUACAAG 83  
Db 23 TGTCCTGCTACTTACTCCAAG 1

RESULT 11  
US-10-490-955-248/c

Sequence 248, Application US/10490955  
Publication No. US20050059005A1  
GENERAL INFORMATION:

APPLICANT: Tuschl, Thomas  
APPLICANT: Lagos-Quintana, Mariana  
APPLICANT: Lendeckel, Winfried  
APPLICANT: Meyer, Jutta  
APPLICANT: Raubut, Reinhard  
TITLE OF INVENTION: MicroRNA Molecules  
FILE REFERENCE: 2923-613  
CURRENT APPLICATION NUMBER: US/10/490,955  
CURRENT FILING DATE: 2004-03-29  
PRIOR APPLICATION NUMBER: PCT/EP02/10881  
PRIOR FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: EP 02 016 772.2  
PRIOR FILING DATE: 2002-07-26  
PRIOR APPLICATION NUMBER: EP 02 006 712.0  
PRIOR FILING DATE: 2002-03-22  
PRIOR APPLICATION NUMBER: EP 01 123 453.1  
PRIOR FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 562  
SOFTWARE: PatentIn version 3.2

SEQ ID NO 248  
LENGTH: 83  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-490-955-248

Query Match 40.2%; Score 33.4; DB 10; Length 83;  
Best Local Similarity 45.8%; Pred. No. 0.15;  
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 1 CCUGAGUAAAGGACGACAUAGGUAUUUGAAGGUGGAGGCCAUU 60  
DB 83 CCTGTATTTTGGAGGACGACATATGGCTGCACCTTTCAAAATCCAAACCATTA 24

QY 61 UGUGCUGCCUCAAUAUACAAG 83  
DB 23 TGTGCTGCTACTTACTCCAAAG 1

## RESULT 12

US-10-490-955-305/c  
Sequence 305, Application US/10490955  
Publication No. US2005005905A1  
GENERAL INFORMATION:  
APPLICANT: Tuschl, Thomas  
APPLICANT: Lagos-Quintana, Mariana  
APPLICANT: Lendeckel, Winfried  
APPLICANT: Meyer, Jutta  
APPLICANT: Rauhut, Reinhard  
TITLE OF INVENTION: MicroRNA Molecules  
FILE REFERENCE: 2923-613  
CURRENT APPLICATION NUMBER: US/10/490,955  
CURRENT FILING DATE: 2004-03-29  
PRIOR APPLICATION NUMBER: PCT/EP02/10881  
PRIOR FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: EP 02 016 772.2  
PRIOR FILING DATE: 2002-07-26  
PRIOR APPLICATION NUMBER: EP 02 006 712.0  
PRIOR FILING DATE: 2002-03-22  
PRIOR APPLICATION NUMBER: EP 01 123 453.1  
PRIOR FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 562  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 305  
LENGTH: 83  
TYPE: RNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: D. melanogaster or H. sapiens or M. musculus or C. elegans or  
OTHER INFORMATION: Hela cells  
US-10-490-955-305

Query Match 40.2%; Score 33.4; DB 10; Length 83;  
Best Local Similarity 45.8%; Pred. No. 0.15;  
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 1 CCUGAGUAAAGGACGACAUAGGUAUUUGAAGGUGGAGGCCAUU 60  
DB 83 CCTGTATTTTGGAGGACGACATATGGCTGCACCTTTCAAAATCCAAACCATTA 24

QY 61 UGUGCUGCCUCAAUAUACAAG 83  
DB 23 TGTGCTGCTACTTACTCCAAAG 1

## RESULT 13

US-11-100-897-72/c  
Sequence 72, Application US/11100897  
Publication No. US20050272075A1  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, Nana  
APPLICANT: Kongsbak, Lars  
APPLICANT: Kaupinen, Sakari

APPLICANT: Echwald, Soren Mergenthaler  
APPLICANT: Mouritzen, Peter  
APPLICANT: Nielsen, Peter Stein  
APPLICANT: Norholm, Mikkel  
TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF MICRORNAs AND SMALL  
TITLE OF INVENTION: INTERFERING RNAs  
FILE REFERENCE: 50287/013004  
CURRENT APPLICATION NUMBER: US/11/100,897  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/648,221  
PRIOR FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: 60/619,291  
PRIOR FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: 60/600,961  
PRIOR FILING DATE: 2004-08-12  
PRIOR APPLICATION NUMBER: 60/590,856  
PRIOR FILING DATE: 2004-07-23  
PRIOR APPLICATION NUMBER: 60/560,148  
PRIOR FILING DATE: 2004-04-07  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 72  
LENGTH: 83  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-100-897-72

Query Match 40.2%; Score 33.4; DB 15; Length 83;  
Best Local Similarity 45.8%; Pred. No. 0.15;  
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 1 CCUGAGUAAAGGACGACAUAGGUAUUUGAAGGUGGAGGCCAUU 60  
DB 83 CCTGTATTTTGGAGGACGACATATGGCTGCACCTTTCAAAATCCAAACCATTA 24

QY 61 UGUGCUGCCUCAAUAUACAAG 83  
DB 23 TGTGCTGCTACTTACTCCAAAG 1

## RESULT 14

US-11-230-992-1/c  
Sequence 1, Application US/11230992  
Publication No. US20060073505A1  
GENERAL INFORMATION:  
APPLICANT: Richard H. Griffee  
APPLICANT: Ravi Jain  
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS EFFECTING  
TITLE OF INVENTION: DROSHA-MEDIATED CLEAVAGE  
FILE REFERENCE: CORE0041US  
CURRENT APPLICATION NUMBER: US/11/230,992  
CURRENT FILING DATE: 2005-09-20  
PRIOR APPLICATION NUMBER: 60/612,059  
PRIOR FILING DATE: 2004-09-21  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 83  
TYPE: RNA  
ORGANISM: H. Sapiens  
US-11-230-992-1

Query Match 40.2%; Score 33.4; DB 16; Length 83;  
Best Local Similarity 45.8%; Pred. No. 0.15;  
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 1 CCUGAGUAAAGGACGACAUAGGUAUUUGAAGGUGGAGGCCAUU 60  
DB 83 CCTGTATTTTGGAGGACGACATATGGCTGCACCTTTCAAAATCCAAACCATTA 24

QY 61 UGUGCUGCCUCAAUAUACAAG 83  
DB 23 TGTGCTGCTACTTACTCCAAAG 1



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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 22:25:14 ; Search time 187.343 Seconds  
(without alignments)  
859,641 Million cell updates/sec

Title: US-10-706-798-1

Perfect score: 83.  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2461376 seqs, 970166171 residues

Total number of hits satisfying chosen parameters: 4922752

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA.New.\*

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	83	US-11-194-055-33	Sequence 33, Appl
2	83	100.0	83	US-11-375-650-1	Sequence 1, Appl
3	83	100.0	347503	US-11-266-748A-23474	Sequence 23474, A
4	79	95.2	108	US-11-194-035-32	Sequence 32, Appl
5	40	48.2	40	US-11-194-055-325	Sequence 325, App
6	40	48.2	40	US-11-194-055-326	Sequence 326, App
7	33.4	40.2	83	US-11-194-055-33	Sequence 33, Appl
8	33.4	40.2	83	US-11-375-650-1	Sequence 1, Appl
9	33.4	40.2	347503	US-11-266-748A-23474	Sequence 23474, A
10	29.6	35.7	108	US-11-194-035-32	Sequence 32, Appl
11	28	33.7	1313	US-10-449-902-754	Sequence 2754, Ap
12	28	33.7	1385	US-10-449-902-28048	Sequence 28048, A
13	28	33.7	5689	US-11-218-305-15842	Sequence 15422, A
14	27.4	33.0	333	US-11-266-748A-268472	Sequence 268472, A
15	27.4	33.0	333	US-11-266-748A-328989	Sequence 328989, A
16	27.2	32.8	98	US-11-194-055-35	Sequence 35, Appl
17	27	32.5	64125	US-10-539-228-350	Sequence 350, App
18	26.8	32.3	3103	US-10-449-902-25833	Sequence 25833, A
19	26.8	32.3	39983	US-10-539-228-538	Sequence 538, App
20	26.4	31.8	1502	US-11-218-305-17846	Sequence 17846, A
21	26.4	31.8	181179	US-11-266-748A-61130	Sequence 61130, A
22	26.2	31.6	810	US-11-434-137-9301	Sequence 9301, Ap
23	26.2	31.6	810	US-11-434-184-9301	Sequence 9301, Ap

C	24	26.2	31.6	810	7	US-11-434-199-9301	Sequence 9301, Ap
C	25	26.2	31.6	810	7	US-11-434-203-9301	Sequence 9301, Ap
C	26	26.2	31.6	813	9	US-11-348-413-7433	Sequence 7433, Ap
C	27	26.2	31.6	228006	6	US-10-540-898-119	Sequence 119, App
C	28	26.2	31.6	2160266	7	US-11-434-137-10967	Sequence 10967, A
C	29	26.2	31.6	2160266	7	US-11-434-184-10967	Sequence 10967, A
C	30	26.2	31.6	2160266	7	US-11-434-199-10967	Sequence 10967, A
C	31	26.2	31.6	2160266	7	US-11-434-203-10967	Sequence 10967, A
C	32	26	31.3	1389	9	US-11-056-355B-1552	Sequence 1552, Ap
C	33	26	31.3	3033	9	US-11-299-805-6399	Sequence 6399, Ap
C	34	25.8	31.1	2085	7	US-11-299-868-1012	Sequence 1012, Ap
C	35	25.8	31.1	2085	9	US-11-056-355B-71883	Sequence 71883, A
C	36	25.8	31.1	88208	6	US-10-669-920-909	Sequence 909, App
C	37	25.8	31.1	88445	6	US-10-539-228-724	Sequence 724, App
C	38	25.8	31.1	174600	6	US-10-540-898-497	Sequence 497, App
C	39	25.4	30.6	1000	8	US-11-266-748A-291747	Sequence 291747, A
C	40	25.4	30.6	1000	8	US-11-266-748A-343176	Sequence 343176, A
C	41	25.4	30.6	1000	8	US-11-266-748A-403264	Sequence 403264, A
C	42	25.4	30.6	1000	8	US-11-266-748A-474310	Sequence 474310, A
C	43	25.4	30.6	2414	8	US-11-293-697-350	Sequence 350, App
C	44	25.4	30.6	3360	8	US-11-217-529-82548	Sequence 82548, A
C	45	25.4	30.6	82374	8	US-11-266-748A-24977	Sequence 24977, A

## ALIGNMENTS

```
RESULT 1
US-11-194-055-33
; Sequence 33, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevgiani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 83
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-33

Query Match 100.0%; Score 83; DB 8; Length 83;
Best Local Similarity 73.5%; Pred. No. 1.2e-20; Indels 0; Gaps 0;
Matches 61; Conservative 22; Mismatches 0;
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QY 1 CCUUGAGUAAUAGUAGCAGCAUAUUGUUGUUGAAAGUUGCAGGCCAUU 60  
DB 1 CTTTGAGTAAATAGAGACATATGCTTGTGATTTGAAAAGTGCAGGCCATAT 60  
QY 61 UGUGCGCCUCAAUUAUACAAG 83

Db 61 TGTGCTGCTCAAAAATACAAAG 83

## RESULT 2

US-11-375-650-1  
; Sequence 1, Application US/11375650  
; Publication No. US20060165659A1  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; APPLICANT: Calin, George A.  
; TITLE OF INVENTION: Compositions and Methods for Cancer  
; TITLE OF INVENTION: Diagnosis and Therapy  
; FILE REFERENCE: 08321-0126US1  
; CURRENT APPLICATION NUMBER: US/11/375,650  
; CURRENT FILING DATE: 2006-03-13  
; PRIOR APPLICATION NUMBER: US/10/706,798  
; PRIOR FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: 60/425,864  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/469,464  
; PRIOR FILING DATE: 2003-05-09  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 83  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-375-650-1

Query Match 100.0%; Score 83; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1,2e-20;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGGAGUAAAGUAGGACCAUUAUGUUGUGAUAUUGGAGGCGCCAUU 60  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 1 CCUGGAGUAAAGUAGGACCAUUAUGUUGUGAUAUUGGAGGCGCCAUU 60  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Qy 61 UGUGGUGCCUCAAUAUACAAG 83  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 61 UGUGGUGCCUCAAUAUACAAG 83  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

## RESULT 3

US-11-266-748A-23474/C  
; Sequence 23474, Application US/11266748A  
; Publication No. US2006013463A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcription Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 23474  
; LENGTH: 347503  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-23474

Query Match 100.0%; Score 83; DB 8; Length 347503;  
Best Local Similarity 73.5%; Pred. No. 2,4e-19;  
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGGAGUAAAGUAGGACCAUUAUGUUGUGAUAUUGGAGGCGCCAUU 60  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 52198 CTTGAGGTAAGTAGGACGACATTAATGTTGTGATTTTGAAAAGTGCGAGCCATAT 52139  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Qy 61 UGUGGUGCCUCAAUAUACAAG 83  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 52138 TGTGCTGCTCAAAAATACAAAG 52116  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

## RESULT 4

US-11-194-055-32  
; Sequence 32, Application US/11194055  
; Publication No. US20060105360A1  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; APPLICANT: Liu, Chang-Gong  
; APPLICANT: Calin, George, A.  
; APPLICANT: Cinzia, Sevigiani  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH  
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL  
; FILE REFERENCE: 3589.1018-008  
; CURRENT APPLICATION NUMBER: US/11/194,055  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: PCT/US2005/004865  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: 60/543,119  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,929  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,929  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,963  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,940  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/580,359  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 60/580,797  
; PRIOR FILING DATE: 2004-06-18  
; NUMBER OF SEQ ID NOS: 663  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 108  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-194-055-32

Query Match 95.2%; Score 79; DB 8; Length 108;  
Best Local Similarity 72.2%; Pred. No. 3,6e-19;  
Matches 57; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGGAGUAAAGUAGGACCAUUAUGUUGUGAUAUUGGAGGCGCCAUU 60  
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Db 30 CTTGAGGTAAGTAGGACGACATTAATGTTGTGATTTTGAAAAGTGCGAGCCATAT 89  
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Qy 61 UGUGGUGCCUCAAUAUACAAG 79  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 90 TGTGCTGCTCAAAAATAC 108  
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## RESULT 5

US-11-194-055-325  
; Sequence 325, Application US/11194055

```
; Publication NO. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Cinzia, George, A.
; APPLICANT: Cinzia, Sevgi
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-11-194-055-325

Query Match      48.2%; Score 40; DB 8; Length 40;
Best Local Similarity 67.5%; Pred. No. 3.9e-05;
Matches 27; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCUGAGUAAAGUAGCAGCAUAUGGUUUUGAGU 40
Db      1 CTTTGAGTAAAGTACGACGACATATGTTGTGATTT 40

RESULT 6
US-11-194-055-326
; Sequence 326, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Cinzia, George, A.
; APPLICANT: Cinzia, Sevgi
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: oligonucleotide probe
US-11-194-055-327
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; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-11-194-055-326

Query Match      48.2%; Score 40; DB 8; Length 40;
Best Local Similarity 65.0%; Pred. No. 3.9e-05;
Matches 26; Conservative 14; Mismatches 0; Indels 0; Gaps 0;

QY      30 UUUGUGAUUUUUAGGUGCAGCCAUUUGUCUGCC 69
Db      1 TTTGTGATTTTGAAGGTCAGGCAATGTGTGCGCC 40

RESULT 7
US-11-194-055-33/c
; Sequence 33, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Cinzia, George, A.
; APPLICANT: Cinzia, Sevgi
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 83
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: oligonucleotide probe
US-11-194-055-33

Query Match      40.2%; Score 33.4; DB 8; Length 83;
Best Local Similarity 45.8%; Pred. No. 0.013;
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY      1 CCUGAGUAAAGUAGCAGCAUAUGGUUUUGAGU 60
Db      83 CTTTGATTTTGGAGCAGCAGATATGCGCTGCACCTTTCAAAATCCAAACATTA 24

QY      61 UUGUCGCGCCUCAAUAUACAGG 83
Db      23 TGTGCTGCTACTTACTCCAGG 1

RESULT 8
US-11-375-650-1/c
; Sequence 1, Application US/11375650
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Publication No. US20060165659A1  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
TITLE OF INVENTION: Compositions and Methods for Cancer  
FILE REFERENCE: 08321-0126US1  
CURRENT APPLICATION NUMBER: US/11/375,650  
PRIOR FILING DATE: 2006-03-13  
PRIOR APPLICATION NUMBER: US/10/706,798  
PRIOR FILING DATE: 2003-11-12  
PRIOR APPLICATION NUMBER: 60/425,864  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: 60/469,464  
PRIOR FILING DATE: 2003-05-09  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 83  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-375-650-1

Query Match 40.2%; Score 33.4; DB 9; Length 83;  
Best Local Similarity 45.8%; Pred. No. 0.013;  
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CCUGGAGUAAAGUAGCACAUAUGGUGUUGAUAAGGUGGACCAU 60  
Db 83 CTTGTATTTTGTGAGGACGACATATGCGCTGACCTTTCAAAATCCAAACATTA 24  
Qy 61 UGUGCGCCUCAAUAUACAAG 83  
Db 23 TGTGCTGCTACTTACTCAAG 1

RESULT 9  
US-11-266-748A-23474  
Sequence 23474, Application US/11266748A  
Publication No. US2006013463A1  
GENERAL INFORMATION:  
APPLICANT: Harkin, Paul  
APPLICANT: Johnston, Patrick  
APPLICANT: Mulligan, Karl  
TITLE OF INVENTION: Transcriptome Microarray Technology and  
FILE REFERENCE: 55815-0102 (319189)  
CURRENT APPLICATION NUMBER: US/11/266,748A  
PRIOR FILING DATE: 2005-11-03  
PRIOR APPLICATION NUMBER: EP 04105479.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105482.6  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105483.4  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105507.0  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105485.9  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105484.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: US 60/662,276  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700,293  
PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 48396  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 23474  
LENGTH: 347503  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-11-266-748A-23474

Query Match 40.2%; Score 33.4; DB 8; Length 347503;  
Best Local Similarity 45.8%; Pred. No. 0.26;  
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CCUGGAGUAAAGUAGCACAUAUGGUGUUGAUAAGGUGGACCAU 60  
Db 52116 CTTGTATTTTGTGAGGACGACATATGCGCTGACCTTTCAAAATCCAAACATTA 52175  
Qy 61 UGUGCGCCUCAAUAUACAAG 83  
Db 52176 TGTGCTGCTACTTACTCAAG 52198

RESULT 10  
US-11-194-055-32/c  
Sequence 32, Application US/11194055  
Publication No. US20060105360A1  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
APPLICANT: Liu, Chang-Gong  
APPLICANT: Calin, George, A.  
APPLICANT: Cinzia, Seviagnani  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH  
TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL  
FILE REFERENCE: 3589,1018-008  
CURRENT APPLICATION NUMBER: US/11/194,055  
PRIOR FILING DATE: 2005-07-29  
PRIOR APPLICATION NUMBER: PCT/US2005/004865  
PRIOR FILING DATE: 2005-02-09  
PRIOR APPLICATION NUMBER: 60/543,119  
PRIOR FILING DATE: 2004-02-09  
PRIOR APPLICATION NUMBER: 60/542,929  
PRIOR FILING DATE: 2004-02-09  
PRIOR APPLICATION NUMBER: 60/542,963  
PRIOR FILING DATE: 2004-02-09  
PRIOR APPLICATION NUMBER: 60/542,940  
PRIOR FILING DATE: 2004-02-09  
PRIOR APPLICATION NUMBER: 60/580,959  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 60/580,797  
PRIOR FILING DATE: 2004-06-18  
NUMBER OF SEQ ID NOS: 663  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 108  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-194-055-32

Query Match 35.7%; Score 29.6; DB 8; Length 108;  
Best Local Similarity 48.5%; Pred. No. 0.34;  
Matches 33; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

Qy 16 GCAGCACAUAUGGUGUUGAUAAGGUGGACCAUAUUGGUGGUCUAAAA 75  
Db 97 GCAGCACAUAUATGCGCTGACCTTTCAAAATCCAAACATTATGTGCTACTTTA 38  
Qy 76 AUAACAAG 83  
Db 37 CTCACAAG 30

RESULT 11  
US-10-449-902-2754  
Sequence 2754, Application US/10449902  
Publication No. US20060123505A1  
GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF



```

; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ. ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2754
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK060554
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-2754

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Query Match 33.7%; Score 28; DB 6; Length 1313;
Best Local Similarity 44.7%; Pred. No. 3.2;
Matches 34; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

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QY 5 GGAGUAAAGUAGCAGCAUAUGUUUGAGUUUUGAAAGUGCGCCAUUUG 64
DB 330 GAAGTGAAGAGATGCGATTATGCTATTAAGATTGTAATGATCAAGCTATATGAA 389
QY 65 CUGCCUCAAUAUACA 80
DB 390 AACCAATTAAGGTAA 405

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RESULT 12
US-10-449-902-28048
; Sequence 28048, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ. ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28048
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK103490
; DATABASE ENTRY DATE: 2002-08-28
; US-10-449-902-28048

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Query Match 33.7%; Score 28; DB 6; Length 1385;
Best Local Similarity 44.7%; Pred. No. 3.3;
Matches 34; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

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QY 5 GGAGUAAAGUAGCAGCAUAUGUUUGAGUUUUGAAAGUGCGCCAUUUG 64
DB 327 GAAGTGAAGAGATGCGATTATGCTATTAAGATTGTAATGATCAAGCTATATGAA 386
QY 65 CUGCCUCAAUAUACA 80
DB 387 AACCAATTAAGGTAA 402

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RESULT 13

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US-11-218-305-15422/C
; Sequence 15422, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaIRD, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ. ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15422
; LENGTH: 5689
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (420)..(420)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: (759)..(759)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-218-305-15422

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Query Match 33.7%; Score 28; DB 9; Length 5689;
Best Local Similarity 42.6%; Pred. No. 5.5;
Matches 29; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

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QY 10 AANGUACGACGACAUUAUGUUUGAGUUUUGAAAGUGCGCCAUUUGCGCC 69
DB 3570 AAAATATCGATGACGAAAGTTTGACATTGCGAAGAAAGACCGAGTTCTCTGGA 3511
QY 70 UCAGAAAU 77
DB 3510 TTGAAACT 3503

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RESULT 14
US-11-266-748A-268472
; Sequence 268472, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

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Title: US-10-706-798-3

Perfect score: 22

Sequence: 1 uagcagcacauaugguugug 22

Scoring table: IDENTITY NUC

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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

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7: gb\_scs:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_hcg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	100.0	22	2	CQ873604	Sequence
2	22	100.0	22	2	CS166305	Sequence
3	22	100.0	22	2	CS185031	Sequence
4	22	100.0	22	2	CS185033	Sequence
5	22	100.0	22	2	CS185099	Sequence
6	22	100.0	22	2	CS185099	Sequence
7	22	100.0	22	6	MMU459705	Sequence
8	22	100.0	40	2	CS185094	Sequence
9	22	100.0	83	2	CS185098	Sequence
10	22	100.0	83	2	CS188802	Sequence
11	22	100.0	108	2	CS188801	Sequence
12	22	100.0	663	5	AY866304	Lemur cat
13	22	100.0	712	5	AY866308	Lagotrix
14	22	100.0	747	5	AY866306	Pongo pyg
15	22	100.0	825	5	AY866302	Saguinus
16	22	100.0	836	5	AY866299	Ateles ge
17	22	100.0	871	5	AY866301	Macaca nu
18	22	100.0	896	5	AY866305	Macaca mu

19	22	100.0	901	5	AY866300	Gorilla g
20	22	100.0	902	5	AY866307	Pan trogl
21	22	100.0	914	5	AY866303	Pan panis
22	22	100.0	153092	5	AC069475	Homo sapi
23	22	100.0	154868	5	AF334404	Homo sapi
24	22	100.0	154887	5	AL137060	Human DNA
25	22	100.0	172152	6	AC154660	Mus muscu
26	22	100.0	184155	12	AC155017	Bos tauru
27	22	100.0	235659	12	AC152429	Bos tauru
28	22	100.0	347503	5	AF279660	Homo sapi
29	22	100.0	350000	5	AF440619	Homo sapi
30	22	92.7	97230	11	AL606727	Zebrafish
31	20.4	92.7	214290	11	BX294379	Zebrafish
32	20	90.9	945	5	HSJA325715	Homo sapi
33	20	90.9	157118	5	AC069286	Homo sapi
34	20	90.9	199906	12	AC021764	Homo sapi
35	19.4	88.2	129966	12	AC148571	Taeniodys
36	19.4	88.2	142102	12	AC149026	Alligator
37	19.4	88.2	145139	12	AC148426	Omnithor
38	19.4	88.2	150820	12	AC154053	Ictalurus
39	19.4	88.2	151543	12	AC148422	Meleagris
40	19.4	88.2	160466	12	AC148572	Taeniodys
41	19.4	88.2	161530	12	CT027989	Danio rer
42	19.4	88.2	222429	12	AC148419	Meleagris
43	19.4	88.2	250743	13	AE014836	Plasmodiu
44	19	86.4	161956	11	BX640540	Chicken D
45	18.8	85.5	883	5	AF330705	Homo sapi

## ALIGNMENTS

RESULT 1	CQ873604	22 bp	RNA	linear	PAT 27-SEP-2004
LOCUS	CQ873604	23	from Patent WO2004076622.		
DEFINITION	Sequence				
ACCESSION	CQ873604				
VERSION	CQ873604.1	GI:52747196			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	1				
AUTHORS	Taira, K. and Kawasaki, H.				
TITLE	Regulation of mammalian cells				
JOURNAL	Patent: WO 2004076622-A 23 10-SEP-2004;				
	National Institute of Advanced Industrial Science and Tec hnology				
	(JP)				
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	/organism="Homo sapiens"				
	/mol_type="unassigned RNA"				
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ORIGIN					
Query Match	100.0%; Score 22; DB 2; Length 22;				
Best Local Similarity	68.2%; Pred. No. 1;				
Matches	15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 UAGCAGCACAUAAUGGUGUG 22				
Db	1 TACGACGACATATGCTTGTG 22				
RESULT 2	CS166305	22 bp	RNA	linear	PAT 26-SEP-2005
LOCUS	CS166305	16	from Patent WO2005078096.		
DEFINITION	Sequence				
ACCESSION	CS166305				
VERSION	CS166305.1	GI:76362075			
KEYWORDS					

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Zamore, P. D.  
TITLE Dual functional oligonucleotides for use in repressing mutant gene expression  
JOURNAL Patent: WO 2005078096-A 16 25-AUG-2005;  
University of Massachusetts (US)  
LOCATION/Qualifiers

FEATURES source  
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/organism="Homo sapiens"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 68.2%; Pred. No. 1;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCAUAUUGUUG 22  
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1 TAGCAGCACAATAATGTTGTG 22

Db

RESULT 3  
CS185031 22 bp DNA linear PAT 01-NOV-2005  
LOCUS CS185031  
DEFINITION Sequence 5 from Patent WO2005098029.  
ACCESSION CS185031  
VERSION CS185031.1 GI:78585003  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
OTHER SEQUENCES; artificial sequences.

REFERENCE 1  
AUTHORS Jacobsen, N.  
TITLE NOVEL METHODS FOR QUANTIFICATION OF MICRORNAS AND SMALL INTERFERING RNAS  
JOURNAL Patent: WO 2005098029-A 5 20-OCT-2005;  
Exiqon A/S (DK)  
LOCATION/Qualifiers

FEATURES source  
1..22  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic sequence"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 68.2%; Pred. No. 1;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCAUAUUGUUG 22  
:|||||||:|:|:|:|:|:  
1 TAGCAGCACAATAATGTTGTG 22

Db

RESULT 4  
CS185033 22 bp RNA linear PAT 01-NOV-2005  
LOCUS CS185033  
DEFINITION Sequence 7 from Patent WO2005098029.  
ACCESSION CS185033  
VERSION CS185033.1 GI:78585005  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
OTHER SEQUENCES; artificial sequences.

REFERENCE 1  
AUTHORS Jacobsen, N.  
TITLE NOVEL METHODS FOR QUANTIFICATION OF MICRORNAS AND SMALL INTERFERING

JOURNAL RNAS  
Patent: WO 2005098029-A 7 20-OCT-2005;  
Exiqon A/S (DK)  
LOCATION/Qualifiers

FEATURES source  
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/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Synthetic sequence"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 68.2%; Pred. No. 1;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCAUAUUGUUG 22  
:|||||||:|:|:|:|:|:  
1 TAGCAGCACAATAATGTTGTG 22

Db

RESULT 5  
CS185099 22 bp RNA linear PAT 01-NOV-2005  
LOCUS CS185099  
DEFINITION Sequence 73 from Patent WO2005098029.  
ACCESSION CS185099  
VERSION CS185099.1 GI:78585071  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Jacobsen, N.  
TITLE NOVEL METHODS FOR QUANTIFICATION OF MICRORNAS AND SMALL INTERFERING RNAS  
JOURNAL Patent: WO 2005098029-A 73 20-OCT-2005;  
Exiqon A/S (DK)  
LOCATION/Qualifiers

FEATURES source  
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/organism="Homo sapiens"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 68.2%; Pred. No. 1;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCAUAUUGUUG 22  
:|||||||:|:~|:|:|:|:~|:  
1 TAGCAGCACAATAATGTTGTG 22

Db

RESULT 6  
HSA421733 22 bp RNA linear PRI 11-JUN-2003  
LOCUS HSA421733  
DEFINITION Homo sapiens microRNA miR-15.  
ACCESSION AJ421733  
VERSION AJ421733.1 GI:17646018  
KEYWORDS miRNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Lagos-Quintana, M., Rauhut, R., Lendeckel, W. and Tuschl, T.  
TITLE Identification of novel genes coding for small expressed RNAs  
JOURNAL Science 294 (5543), 853-858 (2001)  
PUBMED 11679670  
REFERENCE 2 (bases 1 to 22)  
AUTHORS Tuschl, T.

TITLE Direct Submission  
JOURNAL Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck  
Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen  
37077, Germany  
COMMENT Related sequences: AC069475.  
FEATURES Location/Qualifiers  
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1 TAGCAGCATATGTTGTG 22  
Db 1 TAGCAGCATATGTTGTG 22  
RESULT 7  
LOCUS MMU459705 22 bp mRNA linear ROD 05-JUL-2002  
DEFINITION Mus musculus microRNA mir-15a.  
ACCESSION AJ459705  
VERSION AJ459705.1 GI:20799023  
KEYWORDS microRNA mir-15a; mir-15a gene; miRNA.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS 1  
Lagos-Quintana, M., Rauhut, R., Yalcin, A., Meyer, J., Lendeckel, W. and  
Tuschl, T.  
TITLE Identification of tissue-specific microRNAs from mouse  
JOURNAL Curr. Biol. 12 (9), 735-739 (2002)  
PUBMED 12007417  
REFERENCE 2 (bases 1 to 22)  
AUTHORS Tuschl, T.  
TITLE Direct Submission  
JOURNAL Submitted (06-MAY-2002) Dep. of Cellular Biochemistry, Max Planck  
Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen  
37077, Germany  
COMMENT related sequence: T172137197 (Trace Archive).  
FEATURES Location/Qualifiers  
source  
1..22  
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/product="microRNA mir-15a"  
/note="transcribed as larger precursor, predicted to form  
hairpin"  
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Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
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1 TAGCAGCATATGTTGTG 22  
Db 1 TAGCAGCATATGTTGTG 22

RESULT 8  
LOCUS CS189094 40 bp DNA linear PAT 04-NOV-2005  
DEFINITION Sequence 325 from Patent WO2005078139.  
ACCESSION CS189094  
VERSION CS189094.1 GI:80750083  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS 1  
Croce, C.M.  
JOURNAL Patent: WO 2005078139-A 325 25-AUG-2005;  
THOMAS JEFFERSON UNIVERSITY (US)  
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/note="oligonucleotide probe"  
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Best Local Similarity 68.2%; Pred. No. 1.1;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
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14 TAGCAGCATATGTTGTG 35  
Db 14 TAGCAGCATATGTTGTG 35  
RESULT 9  
LOCUS CS185098 83 bp RNA linear PAT 01-NOV-2005  
DEFINITION Sequence 72 from Patent WO2005098029.  
ACCESSION CS185098  
VERSION CS185098.1 GI:78585070  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
AUTHORS 1  
Jacobsen, N.  
TITLE NOVEL METHODS FOR QUANTIFICATION OF MICRORNAs AND SMALL INTERFERING  
JOURNAL RNAs  
PATENT: WO 2005098029-A 72 20-OCT-2005;  
EXIGON A/S (DK)  
FEATURES Location/Qualifiers  
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Best Local Similarity 68.2%; Pred. No. 1.2;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
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14 TAGCAGCATATGTTGTG 35  
Db 14 TAGCAGCATATGTTGTG 35  
RESULT 10  
LOCUS CS188802 83 bp DNA linear PAT 04-NOV-2005  
DEFINITION Sequence 33 from Patent WO2005078139.  
ACCESSION CS188802  
VERSION CS188802.1 GI:80749791  
KEYWORDS  
SOURCE  
Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Croce,C.M.  
JOURNAL Patent: WO 2005078139-A 33 25-AUG-2005;  
THOMAS JEFFERSON UNIVERSITY (US)

FEATURES  
source 1..83  
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/mol\_type="unassigned DNA"  
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ORIGIN  
Query Match 100.0%; Score 22; DB 2; Length 83;  
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Qy 1 UAGCAGCACAUAAUGUUUG 22  
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14 TAGCAGCACATATAGCTTTGTG 35

RESULT 11  
LOCUS CS188801 108 bp DNA linear PAT 04-NOV-2005  
DEFINITION Sequence 32 from Patent WO2005078139.  
ACCESSION CS188801  
VERSION CS188801.1 GI:80749790  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Croce,C.M.  
JOURNAL Patent: WO 2005078139-A 32 25-AUG-2005;  
THOMAS JEFFERSON UNIVERSITY (US)

FEATURES  
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Qy 1 UAGCAGCACAUAAUGUUUG 22  
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43 TAGCAGCACATATAGCTTTGTG 64

RESULT 12  
LOCUS AY866304 663 bp DNA linear PRI 24-JAN-2005  
DEFINITION Lemur catla microRNA mir-15a and microRNA mir-16-1 genes, complete  
sequence.  
ACCESSION AY866304  
VERSION AY866304  
KEYWORDS  
SOURCE Lemur catla (ring-tailed lemur)  
ORGANISM Lemur catla  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirhini;  
Lemnidae; Lemur.

REFERENCE 1 (bases 1 to 663)  
AUTHORS Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H. and Cuppen,E.  
Phylogenetic Shadowing and Computational Identification of Human

TITLE

JOURNAL microRNA Genes  
Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE 2 (bases 1 to 663)  
AUTHORS Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H.A. and Cuppen,E.

TITLE Direct Submission  
JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalaan 8, Utrecht  
3584 CT, The Netherlands

FEATURES  
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/note="based on Homo sapiens mir-15a"  
463..484  
/product="microRNA mir-15a"  
590..663  
/product="precursor microRNA mir-16-1"  
/note="based on Homo sapiens mir-16-1"  
603..624  
/product="microRNA mir-16-1"

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Best Local Similarity 68.2%; Pred. No. 1.6;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGUUUG 22  
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463 TAGCAGCACATATAGCTTTGTG 484

RESULT 13  
LOCUS AY866308 712 bp DNA linear PRI 24-JAN-2005  
DEFINITION Lagotrix lagotricha microRNA mir-15a and microRNA mir-16-1 genes,  
complete sequence.  
ACCESSION AY866308  
VERSION AY866308  
KEYWORDS  
SOURCE Lagotrix lagotricha (common woolly monkey)  
ORGANISM Lagotrix lagotricha  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;  
Cebidae; Ateleinae; Lagotrix.

REFERENCE 1 (bases 1 to 712)  
AUTHORS Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H., and Cuppen,E.

TITLE Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
JOURNAL Cell 120 (1), 21-24 (2005)  
PUBMED 15652478  
REFERENCE 2 (bases 1 to 712)  
AUTHORS Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,  
Plasterk,R.H.A. and Cuppen,E.

TITLE Direct Submission  
JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaalaan 8, Utrecht  
3584 CT, The Netherlands

FEATURES  
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/note="based on Homo sapiens mir-15a"  
403..424  
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530..618  
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misc\_RNA /note="based on Homo sapiens mir-16-1"  
543..564  
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ORIGIN

Query Match 100.0%; Score 22; DB 5; Length 712;  
Best Local Similarity 68.2%; Pred. No. 1.6;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGACAUAUGGUGUG 22  
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Db 403 TAGCAGCACATATGCTTGTG 424

RESULT 14  
AY866306 747 bp DNA linear PRI 24-JAN-2005  
LOCUS Pongo pygmaeus microRNA mir-15a and microRNA mir-16-1 genes,  
DEFINITION complete sequence.  
ACCESSION AY866306  
VERSION AY866306.1 GI:57903108  
KEYWORDS  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Pongo.  
REFERENCE 1 (bases 1 to 747)  
Berezikov E., Gurjev V., van de Belt J., Wienholds E.,  
Plasterk R.H. and Cuppen E.,  
Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
Cell 120 (1), 21-24 (2005)  
15652478  
2 (bases 1 to 747)  
Berezikov E., Gurjev V., van de Belt J., Wienholds E.,  
Plasterk R.H.A. and Cuppen E.,  
Direct Submission  
Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht  
3584 CT, The Netherlands

FEATURES  
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1..747  
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617..705  
/product="precursor microRNA mir-16-1"  
/note="based on Homo sapiens mir-16-1"  
630..651  
/product="microRNA mir-16-1"

ORIGIN

Query Match 100.0%; Score 22; DB 5; Length 747;  
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Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGACAUAUGGUGUG 22  
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Db 490 TAGCAGCACATATGCTTGTG 511

RESULT 15  
AY866302 825 bp DNA linear PRI 24-JAN-2005  
LOCUS Saginus labiatus microRNA mir-15a and microRNA mir-16-1 genes,  
DEFINITION complete sequence.  
ACCESSION AY866302  
VERSION AY866302.1 GI:57903104

KEYWORDS  
SOURCE Saginus labiatus (red-cheeked mustached tamarin)  
ORGANISM Saginus labiatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Placryrhini;  
Catheriidae; Saginus.

REFERENCE 1 (bases 1 to 825)  
Berezikov E., Gurjev V., van de Belt J., Wienholds E.,  
Plasterk R.H. and Cuppen E.,  
Phylogenetic Shadowing and Computational Identification of Human  
microRNA Genes  
Cell 120 (1), 21-24 (2005)  
15652478  
2 (bases 1 to 825)  
Berezikov E., Gurjev V., van de Belt J., Wienholds E.,  
Plasterk R.H.A. and Cuppen E.,  
Direct Submission  
Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht  
3584 CT, The Netherlands

FEATURES  
source  
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588..676  
/product="precursor microRNA mir-16-1"  
/note="based on Homo sapiens mir-16-1"  
601..622  
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ORIGIN

Query Match 100.0%; Score 22; DB 5; Length 825;  
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QY 1 UAGCAGACAUAUGGUGUG 22  
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Search completed: November 1, 2006, 20:59:42  
Job time : 492.143 secs

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C	1	22	100.0	330	14	DR22A19S	AL733377	Danio rerio
C	2	22	100.0	486	11	AQ672199	AQ672199	HS_2151_E
C	3	22	100.0	638	11	A2938498	2M0197A08	A2938498
C	4	19.4	88.2	445	4	BW837082	BW837082	BW837082
C	5	19.4	88.2	627	2	BJ627722	BJ627722	BJ627722
C	6	19.4	88.2	723	9	CX379068	CX379068	JGI_XZT50
C	7	19.4	88.2	785	4	BW723290	BW723290	BW723290
C	8	19.4	88.2	804	4	BW301170	BW301170	BW301170
C	9	19.4	88.2	884	3	BU909485	BU909485	AGNCNCURT
C	10	18.8	85.5	394	13	CL270436	CL270436	Ggal_1056
C	11	18.8	85.5	586	11	BH048477	BH048477	RCEI-24-3
C	12	18.8	85.5	830	4	CB562036	CB562036	AGNCNCURT
C	13	18.8	85.5	893	14	CNS032XX	AL222438	Tetradodon
C	14	18.4	83.6	348	10	DS975958	DS975958	SKin-13_E
C	15	18.4	83.6	932	1	AL634787	AL634787	AL694787
C	16	17.8	80.9	191	1	AI634347	AI634347	ts96b02.x
C	17	17.8	80.9	386	11	AO892377	AO892377	HS_3112_E
C	18	17.8	80.9	421	11	AO186977	AO186977	HS_3122_E
C	19	17.8	80.9	422	8	CX082256	CX082256	EHAT87TR

C	20	17.8	80.9	473	8	CV473806	1	D
C	21	17.8	80.9	559	8	CX088035		
C	22	17.8	80.9	604	8	CX089370		
C	23	17.8	80.9	613	14	DE135052		
C	24	17.8	80.9	617	13	CZ079893	0	Ba007
C	25	17.8	80.9	631	8	CX097110		
C	26	17.8	80.9	670	14	CR061257		
C	27	17.8	80.9	679	11	AZ428541		
C	28	17.8	80.9	764	13	DU459257		
C	29	17.8	80.9	802	4	BX887642		
C	30	17.8	80.9	804	13	CW837931		
C	31	17.8	80.9	823	11	BH161771		
C	32	17.8	80.9	860	11	AZ678560		
C	33	17.8	80.9	889	11	AZ684626		
C	34	17.8	80.9	983	11	BH164645		
C	35	17.8	80.9	1222	2	B1869305		
C	36	17.4	79.1	260	13	CM401759		
C	37	17.4	79.1	271	4	BX688587		
C	38	17.4	79.1	364	12	CE710553		
C	39	17.4	79.1	412	4	CB617339		
C	40	17.4	79.1	420	1	AL119702	DKEFD7610	
C	41	17.4	79.1	459	3	BP085372		
C	42	17.4	79.1	500	1	AU086235		
C	43	17.4	79.1	543	2	BG410941	EM1_27_H0	
C	44	17.4	79.1	611	11	BH059786	PC1-24-3	
C	45	17.4	79.1	627	13	CM112106	CM112106_104_485_1	

## ALIGNMENTS

RESULT 1	
DR22A19S	
LOCUS	330 bp
DEFINITION	DNA linear GSS 27-NOV-2002
	Danio rerio genomic clone DKEY-22A19, genomic survey sequence.

ACCESSION VERSION	KEYWORDS	SOURCE	ORGANISM
AL738377	GI:21248782	GSS:	
AL738377.1		Danio rerio (zebrafish)	
		Danio rerio	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	

REFERENCE	AUTHORS
1 (bases 1 to 330)	Humphray, S.J., Huckle, E. and Hunt, S.E.

**JOURNAL TITLE** Direct Submission  
**SUBMITTED** (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:

COMMENT  
humquery@sanger.ac.uk Unpublished  
this sequence was generated from the SP6 end of BAC 22A19. 22A19 is  
part of the Dattokey BAC Library created by R. Plasterc and N.V.  
Keygene.  
Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).

FEATURES	location/Qualifiers
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/issue_type="Pestis"
/note="Vector pIndigoBAC-536

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ORIGIN	Query Match	100.0%	Score 22	DB 14	Length 330
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Best Local Similarity 68.2%; Pred. No. 6,6;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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Db 162 TAGCAGCACAATAATGTTGTG 183

## RESULT 2

AO672199/c 486 bp DNA linear GSS 24-JUN-1999  
LOCUS HS.2151.B1.B12.MR.CIT.Approved.Human.Genomic.Sperm.Library.D.Homo.sapiens.genomic.clone.Plasmid=2151.Col=23.Row=D,genomic.survey  
sequence.  
ACCESSION AO672199.1 GI:5204870  
VERSION AO672199.1  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 486)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
JOURNAL 10449764  
PUBMED  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@reagen.com).  
BAC end Web Server: http://www.htsc.washington.edu  
Plate: 2151 row: D column: 23  
Seq primer: M13 Reverse  
Class: BAC ends  
High quality sequence stop: 486.  
FEATURES  
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/sex="male"  
/clone\_lib="CIT.Approved.Human.Genomic.Sperm.Library.D"  
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"  
ORIGIN  
Query Match 100.0%; Score 22; DB 11; Length 486;  
Best Local Similarity 68.2%; Pred. No. 6.9;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
OY 1 UAGCAGCACAUAUGUUUG 22  
Db 427 TAGCAGCATATATGTTGTG 406  
RESULT 3  
AZ938498/c 638 bp DNA linear GSS 26-APR-2001  
LOCUS 2M0197A088.Mouse.10kb.plasmid.UUCG2M.library.Mus.musculus.genomic  
clone.UUCG2M0197A08.F,genomic.survey.sequence.  
ACCESSION AZ938498  
VERSION AZ938498.1 GI:13798291  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 638)  
AUTHORS Dunn,D., Acyagci,A., Barber,M., Baecorn,T., Duval,B., Hamill,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL plasmid inserts  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0197 row: 8 column: 08  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 638.  
FEATURES  
source  
1..638  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCG2M0197A08"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUCG2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
ORIGIN  
Query Match 100.0%; Score 22; DB 11; Length 638;  
Best Local Similarity 68.2%; Pred. No. 7.1;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
OY 1 UAGCAGCACAUAUGUUUG 22  
Db 188 TAGCAGCATATATGTTGTG 167  
RESULT 4  
BM837082 445 bp mRNA linear EST 24-DEC-2005  
LOCUS BM837082  
DEFINITION BM837082 Amphioxus Branchiostoma floridae unpublished cDNA library, larva whole animal Branchiostoma floridae cDNA clone b1v059118 3', mRNA sequence.  
ACCESSION BM837082  
VERSION BM837082.1 GI:66445298  
KEYWORDS EST.  
SOURCE Branchiostoma floridae (Florida lancelet)  
ORGANISM Branchiostoma floridae  
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.  
REFERENCE 1 (bases 1 to 445)  
AUTHORS Yu,J., Holland,L.Z., Shin-I,T., Kohara,Y., Satou,Y. and Satoh,N.  
TITLE Expressed genes in Branchiostoma floridae  
JOURNAL Unpublished (2005)

## COMMENT

Contact: Tadaeu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp  
If you want to have a cDNA clone for this EST or if you have any questions, please send an e-mail to Nori Satoh (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou (yutaka@ascidian.zool.kyoto-u.ac.jp).

## FEATURES

## source

1..445  
/organism="Branchiostoma floridae"  
/mol\_type="mRNA"  
/db\_xref="taxon:7739"  
/clone="bf1y059i18"  
/tissue\_type="whole animal"  
/dev\_stage="larva"  
/clone\_lib="Amphioxus Branchiostoma floridae unpublished cDNA library, larva whole animal"

## ORIGIN

Query Match 88.2%; Score 19.4; DB 4; Length 445;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 2 AGCAGCACAAUAGUGUUGU 22

Db 56 AGCAGTACATATATGGTTGTG 76

RESULT 5  
LOCUS B0627722 627 bp mRNA linear EST 01-OCT-2003  
DEFINITION B0627722 NIBB Mochii normalized Xenopus early gastrula library  
Xenopus laevis cDNA clone XL219C06 5', mRNA sequence.

ACCESSION B0627722  
VERSION B0627722.1 GI:37274592  
KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 627)  
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and

## REFERENCE

## AUTHORS

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and

## TITLE

Expressed genes in X. laevis embryo

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Tadaeu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp  
The information of this clone is available through the following URL.  
http://xenopus.nibb.ac.jp.  
Location/Qualifiers

## FEATURES

## source

1..627  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="XL219C06"  
/tissue\_type="whole embryo"  
/dev\_stage="stage 10.5"  
/clone\_lib="NIBB Mochii normalized Xenopus early gastrula library"

## ORIGIN

Query Match 88.2%; Score 19.4; DB 2; Length 627;

Best Local Similarity 61.9%; Pred. No. 1.4e+02;  
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

OY 1 UAGCAGCACAAUAGUGUUGU 21

Db 200 TAGCAGCACATCATGTTGT 220

RESULT 6  
LOCUS CX379068 723 bp mRNA linear EST 08-SEP-2005  
DEFINITION JGI XZT50833 fwd NIH XGC\_tropTad5 Xenopus tropicalis cDNA clone  
IMAGE:7625775 5', mRNA sequence.

ACCESSION CX379068  
VERSION CX379068.2 GI:74290621  
KEYWORDS EST.

SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 723)  
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,

## REFERENCE

## AUTHORS

Brokstein, P. and Lindquist, E.A.  
DOE Joint Genome Institute Xenopus tropicalis EST project  
Unpublished (2004)  
On Jan 5, 2005 this sequence version replaced gi:57147625.  
Contact: Lindquist, E.A., Richardson, P.  
DOE Joint Genome Institute  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925 296 5600  
Fax: 925 296 5710

## JOURNAL

## COMMENT

Email: cdna@jgi-psf.org  
Tissue Procurement: Richard M. Harland laboratory, University of California, Berkeley: http://tropicalis.berkeley.edu/home  
cDNA library Preparation: Richard M. Harland laboratory, University of California, Berkeley  
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  
Clone Distribution: I.M.A.G.E. Consortium/LLNL:  
http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
Plate: XZT 0529 row: b column: 13  
High quality sequence stop: 668.

## FEATURES

## source

Location/Qualifiers  
1..723  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7625775"  
/tissue\_type="whole embryo"  
/dev\_stage="Tadpole (st. 36-41)"  
/lab\_host="E. coli XL1-Blue derivative, Stratagene Electropen-Blue"  
/clone\_lib="NIH XGC\_tropTad5"  
/note="Vector: PCS108; Site 1: SalI; Site 2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector PCS108 (http://mc.berkeley.edu/labs/harland/pages/plasmids.html)"

## ORIGIN

Query Match 88.2%; Score 19.4; DB 9; Length 723;  
Best Local Similarity 61.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

OY 1 UAGCAGCACAAUAGUGUUGU 21

:|||||||||:|||||:

Db	175	TAGCAGCATCATCATGTTTGT	195	
RESULT 7				
LOCUS	BW723290		785 bp	mRNA
DEFINITION	BW723290 Amphioxus Branchiostoma floridae unpublished cDNA library,			
	adult whole animal Branchiostoma floridae cDNA clone bfad05b06 3',			
	mRNA sequence.			
ACCESSION	BW723290			
VERSION	BW723290.1	GI:66309882		
KEYWORDS	EST.			
SOURCE	Branchiostoma floridae (Florida lancelet)			
ORGANISM	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;			
	Branchiostoma.			
REFERENCE	1 (bases 1 to 785)			
AUTHORS	Yu,J., Holland,L.Z., Shin-I,T., Kohara,Y., Satou,Y. and Satoh,N.			
TITLE	Expressed genes in Branchiostoma floridae			
JOURNAL	Unpublished (2005)			
COMMENT	Contact: Tadasu Shin-i			
	Center For Genetic Resource Information			
	National Institute of Genetics			
	111 Yata, Mishima, Shizuoka 411-8540, Japan			
	Tel: 81-559-81-6856			
	Fax: 81-559-81-6855			
	Email: tshin@genes.nig.ac.jp			
	If you want to have a cDNA clone for this EST or if you have any			
	questions, please send an e-mail to Nori Satoh			
	(satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou			
	(yutaka@ascidian.zool.kyoto-u.ac.jp).			
FEATURES	Location/Qualifiers			
source	1..785			
	/organism="Branchiostoma floridae"			
	/mol_type="mRNA"			
	/db_xref="taxon:7739"			
	/clone="bfad05b06"			
	/tissue_type="whole animal"			
	/dev_stage="adult"			
	/clone_lib="Amphioxus Branchiostoma floridae unpublished			
	cDNA library, adult whole animal"			
ORIGIN				
Query Match	88.2%;	Score 19.4;	DB 4;	Length 785;
Best Local Similarity	66.7%;	Pred. NO. 1.5e+02;		
Matches	14; Conservative	6; Mismatches	1;	Indels 0; Gaps 0;
Cy	2 AGCAGCACAAUAGGCUUG 22			
Db	63 AGCAGTACATATGTTTGTG 83			
RESULT 8				
LOCUS	BW730170		804 bp	mRNA
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA library,			
	adult whole animal Branchiostoma floridae cDNA clone bfad05g14 3',			
	mRNA sequence.			
ACCESSION	BW730170			
VERSION	BW730170.1	GI:66316782		
KEYWORDS	EST.			
SOURCE	Branchiostoma floridae (Florida lancelet)			
ORGANISM	Branchiostoma floridae			
	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;			
	Branchiostoma.			
REFERENCE	1 (bases 1 to 804)			
AUTHORS	Yu,J., Holland,L.Z., Shin-I,T., Kohara,Y., Satou,Y. and Satoh,N.			
TITLE	Expressed genes in Branchiostoma floridae			
JOURNAL	Unpublished (2005)			
COMMENT	Contact: Tadasu Shin-i			
	Center For Genetic Resource Information			
	National Institute of Genetics			
	111 Yata, Mishima, Shizuoka 411-8540, Japan			

```

Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
If you want to have a cDNA clone for this EST or if you have any
questions, please send an e-mail to Nori Satoh
(satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
(yutaka@ascidian.zool.kyoto-u.ac.jp).

FEATURES
      source
          1..804
              /organism="Branchiostoma floridae"
              /mol_type="mRNA"
              /db_xref="taxon:7739"
              /clone="bfad054q14"
              /tissue_type="whole animal"
              /dev_stage="adult"
              /clone_id="Amphioxus Branchiostoma floridae unpublished
cDNA library, adult whole animal"

ORIGIN
      Query Match      88.2%; Score 19.4; DB 4; Length 804;
      Best Local Similarity 66.7%; Pred. No. 1.5e+02;
      Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

      Oy
          2 AGCAGCACAAUAGUGUUGUG 22
              ||||| ||||| ||||| |||||
              66 AGCAGTACATATGTTGTG 86

      Db

RESULT 9
BU909485      884 bp      mRNA      linear      EST 17-OCT-2002
LOCUS
DEFINITION
AGNCNCOURT 10481253 NICHG_XGC_Eml1 Xenopus laevis cDNA clone
IMAGE:6635141 5', mRNA sequence.
BU909485
BU909485.1 GI:24091399
EST.
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 884)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Martha Rabbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: LLM14208 row: n column: 05
High quality sequence stop: 633.
location/Qualifiers
    1..884
        /organism="Xenopus laevis"
        /mol_type="mRNA"
        /db_xref="taxon:8355"
        /clone="IMAGE:6635141"
        /tissue_type="embryo (stage 10)"
        /lab_host="DH10B (phage-resistant)"
        /clone_id="NICHG_XGC Eml1"
        /note="vector: pCMV-SF0RT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectional. Primer: Oligo dT. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."

ORIGIN
Query Match      88.2%; Score 19.4; DB 3; Length 884;

```

Best Local Similarity 61.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAUGGUGUGU 21  
:|||||:|||||:  
Db 185 TAGCAGCACAATCATGTTGT 205

RESULT 10  
CL270436/c  
DEFINITION Ggal\_105a PR B06 Ggal PR-1 Gallus gallus genomic clone  
ACCESSION CL270436  
VERSION CL270436.1 GI:58747778  
KEYWORDS GSS.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 394)  
Wicker, T., Robertson, J.S., Schulze, S.R., Feltus, F.A., Magini, V.,  
Morrison, J.A., Mardis, E.R., Wilson, R.K., Peterson, D.G.,  
Peterson, A.H., and Ivarte, R.  
The repetitive landscape of the chicken genome  
Genome Res. 15 (1), 126-136 (2005)  
15256510  
Contact: Peterson AH  
Plant Genome Mapping Laboratory  
University of Georgia, Center for Applied Genetic Technologies  
Riverbend Research Laboratory, Room 162, 110 Riverbend Road,  
Athens, GA 30602 USA  
Tel: 7065830169  
Fax: 7065830160  
Email: paterah@uga.edu  
Sequence from middle repetitive (MR) Cot fraction, Cot 10-100  
Class: Hydroxyapatite-fractionated DNA.  
Location/Qualifiers  
1..394  
/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9031"  
/clone="Ggal\_105a\_PR\_B06"  
/sex="female"  
/clone\_lib="Ggal\_PR-1"  
/note="Produced by Cot-based cloning and sequencing  
(CBCS)"

ORIGIN

Query Match 85.5%; Score 18.8; DB 13; Length 394;  
Best Local Similarity 63.6%; Pred. No. 2.8e+02;  
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAUGGUGUGU 22  
:|||||:|||||:|||||:  
Db 170 TAGAAGCAGCAATGATGTTGTG 149

RESULT 11  
BH048477/c  
LOCUS BH048477 586 bp DNA linear GSS 17-JUL-2001  
DEFINITION RPI-24-346015, TV RPI-24 Mus musculus genomic clone  
ACCESSION BH048477  
VERSION BH048477.1 GI:14836401  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 586)

REFERENCE

AUTHORS Zhao, S., Niernman, W., Malek, J., Sharsman, S., Akinret, B., Levins, M.,  
Teagay, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,  
Russell, D., de Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from Library RPI-24  
Unpublished (1999)  
Other GSSs: RPI-24-346015.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPI-24. For BAC  
library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org). Clones may be purchased from BACPAC  
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end  
page: [http://www.tigr.org/tigr/bac/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tigr/bac/bac_ends/mouse/bac_end_intro.html)  
Plate: 346 row: 0 column: 15  
Seq primer: T7  
Class: BAC ends.  
Location/Qualifiers  
1..586  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPI-24-346015"  
/sex="Male"  
/cell\_type="Spleen/Brain"  
/clone\_lib="RPI-24"  
/note="Vector: pTARPA1; Site\_1: BamHI, Site\_2: BamHI;  
RPI-24 Mouse BAC library produced by Pieter de Jong. The  
library was cloned in the pTARPA1 cloning vector at the  
BamHI sites using MboI partially digested male C57BL/6J  
DNA."

ORIGIN

Query Match 85.5%; Score 18.8; DB 11; Length 586;  
Best Local Similarity 59.1%; Pred. No. 2.9e+02;  
Matches 13; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAUGGUGUGU 22  
:|||||:|||||:|||||:  
Db 321 TAACAGCATAATGATGTTGTG 300

RESULT 12  
CB562036  
LOCUS CB562036 830 bp mRNA linear EST 02-APR-2003  
DEFINITION AGENCOURT 13324904 NICHD XGC Tadi xenopus laevis cDNA clone  
IMAGE:6880576 3', mRNA sequence.  
ACCESSION CB562036  
VERSION CB562036.1 GI:29481566  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 830)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Drs. Donald Brown and Liqun Cai  
cDNA Library Preparation: CLONTECH  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LIML at:

REFERENCE

http://image.lnl.gov  
Plate: LILCM3124 row: d column: 15  
High quality sequence stop: 614.  
Location/Qualifiers

## FEATURES

source

1. 830  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:6880576"  
/dev\_stage="metamorphosis stage 53"  
/clone\_lib="NICHID\_XGC\_Tad1"  
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;  
Site 1: Sfi; Site 2: Sfi; 5' and 3' adaptors were used in  
cloning as follows: 5' adaptor sequence:  
5'-CACGGCCATTAATGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGAGCGGCACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G or T). Average insert size 1.6 kb  
(range 0.9-3.0 kb). 15/15 colonies contained inserts by  
PCR. This library was enriched for full-length clones and  
was constructed by Clontech Laboratories (Palo Alto, CA)."

## ORIGIN

Query Match 85.5%; Score 18.8; DB 4; Length 830;  
Best Local Similarity 59.1%; Pred. No. 3e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 13; Conservative 7;

## Oy

1 UAGCAGCACAUAVUGUUUG 22  
336 TTGACGACATCATATGCTTTG 357

## RESULT 13

CNS032XX 893 bp DNA linear GSS 01-SEP-2000  
LOCUS CNS032XX  
DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone  
207L24 of library G from Tetradon nigroviridis, genomic survey  
sequence.

ACCESSION AL225438.1 GI:7884333  
VERSION AL225438.1  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetradon nigroviridis  
ORGANISM Tetradon nigroviridis  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE 1  
Roest Crolius,H., Jallion,O., Dasiya,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fitzmes,C., Wincker,P., Brothier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
Estimate of human gene number provided by genome-wide analysis  
using Tetradon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)

## REFERENCE

AUTHORS

Roest Crolius,H., Jallion,O., Dasiya,C., Ozouf-Costez,C.,  
Fitzmes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,  
Saurin,W., Bernot,A. and Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetradon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)

## JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

source

1. 893  
/organism="Tetradon nigroviridis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:99883"  
/clone="207L24"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COAG207DF12LP1  
end : T7"

## ORIGIN

Query Match 85.5%; Score 18.8; DB 14; Length 893;  
Best Local Similarity 63.6%; Pred. No. 3e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 14; Conservative 6;

## Oy

1 UAGCAGCACAUAVUGUUUG 22  
631 TAGCAGCACGGAATGTTTG 652

## RESULT 14

DR975958/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

DR975958 348 bp mRNA linear EST 03-JAN-2006  
Skin-13 B03\_pDNR-LIB-SPLA A. transmontanus skin express library  
Acipenser transmontanus cDNA, mRNA sequence.  
DR975958  
DR975958.1 GI:84178869  
EST.  
Acipenser transmontanus (white sturgeon)  
Acipenser transmontanus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;  
Acipenser.  
1 (bases 1 to 348)  
Mariani,V., Mallinverni,R. and Giuffra,E.  
Transcriptome analysis of the American sturgeon (Acipenser  
transmontanus): pathways of gene expression in the spleen and skin  
Unpublished (2005)  
Contact: Valentina Mariani  
Livestock Genomics 1  
PRP-CERSA  
Via Einstein, Loc. Ca.na Codazza, 26900 Lodi (LO), Italy  
Email: valentina.mariani@tecnoparco.org.

## FEATURES

source

1. 348  
/organism="Acipenser transmontanus"  
/mol\_type="mRNA"  
/db\_xref="taxon:7904"  
/clone\_lib="A. transmontanus skin express library"  
/note="Organ: skin"  
Location/Qualifiers

## ORIGIN

Query Match 83.6%; Score 18.4; DB 10; Length 348;  
Best Local Similarity 65.0%; Pred. No. 4.3e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 13; Conservative 6;

## Oy

1 UAGCAGCACAUAVUGUUUG 20  
229 TAGCAGCACATCATGTTTG 210

## RESULT 15

AL694787/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AL694787 932 bp mRNA linear EST 21-MAR-2002  
AL694787 NAPI Anopheles gambiae cDNA clone NAPI-P23-F-06-5, mRNA  
sequence.  
AL694787  
AL694787.1 GI:19614493  
EST.  
Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Culicidae; Anophelinae; Anopheles.

REFERENCE 1 (bases 1 to 932)  
 AUTHORS Christophides,G.K., Blass,K., Zdobnov,E.M., Carmouche,R., Benes,V.  
 TITLE Anopheles gambiae EST, European Molecular Biology Laboratory  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Christophides GK  
 Fotis C. Kafatos Laboratory  
 European Molecular Biology Laboratory  
 Meyerhofstrasse 1, 69117 Heidelberg, Germany  
 Tel: +49 6221 387-440  
 Fax: +49 6221 387-306  
 Email: christophe@embl-heidelberg.de  
 Plate: P23 row: F Column: 06.

FEATURES  
 source 1..932  
 Location/Qualifiers  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7165"  
 /clone="NAP1-P23-F-06-5"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="NAP1"  
 /note="Vector: pRTT3D-PacI; Site 1: NotI; Site 2: EcoRI;  
 ESTs sequenced from the T7 priming site that reads from  
 the 5' end of cDNA. The NAP1 is a directionally cloned and  
 normalized, oligo-T primed cDNA library constructed from a  
 mixture of Anopheles gambiae developmental stages  
 according to: Bonaldo, Lennon & Soares (1996):  
 Normalization and Subtraction: Two Approaches To  
 Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN

Query Match 83.6%; Score 18.4; DB 1; Length 932;  
 Best Local Similarity 65.0%; Pred. No. 4.8e+02;  
 Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AGCAGCACAUAAUGGCUUGU 21  
 |||||:|:|:|:  
 Db 297 AGCAGCACATATGCGTTTGT 278

Search completed: November 1, 2006, 22:21:01  
 Job time : 1026.17 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 19:02:55 ; Search time 105.39 Seconds  
(without alignments)  
1455.440 Million cell updates/sec

Title: US-10-706-798-3

Perfect score: 1 usgcagcacacaauguuugug 22

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: N\_Geneseq\_8:\*  
2: geneseqn1980s:\*  
3: geneseqn1990s:\*  
4: geneseqn2000s:\*  
5: geneseqn2001as:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	8 ADA00084	Ada00084 Human miR
2	22	100.0	22	8 ADA00122	Ada00122 Mouse miR
3	22	100.0	22	12 ADO17091	Ado17091 Human miR
4	22	100.0	22	12 ADP84065	Adp84065 Small nuc
5	22	100.0	22	13 ADR83121	Adr83121 Human miR
6	22	100.0	22	14 ADX03284	Adx03284 Antisense
7	22	100.0	22	14 ADX03184	Adx03184 Human miR
8	22	100.0	22	14 ADY30915	Ady30915 Micro RNA
9	22	100.0	22	14 ADX85423	Adx85423 Human miR
10	22	100.0	22	14 ADZ20390	Adz20390 Human hem
11	22	100.0	22	14 AEC36205	Aec36205 Nucleotid
12	22	100.0	22	14 AED35921	Aed35921 Hsa-miR-1
13	22	100.0	22	14 AED35925	Aed35925 Hsa-miR-1
14	22	100.0	22	14 AED35991	Aed35991 Human miR
15	22	100.0	22	14 AED53385	Aed53385 Human tar
16	22	100.0	22	14 AED53470	Aed53470 Mouse tar
17	22	100.0	22	14 AEB04383	Aeb04383 Mouse miR
18	22	100.0	22	14 AEB04287	Aeb04287 Human miR

19	22	100.0	22	15 AEE26704	Aee26704 Hsa miR-1
20	22	100.0	22	15 AEE26638	Aee26638 hsa-miR-1
21	22	100.0	22	15 AEE26636	Aee26636 hsa-miR-1
22	22	100.0	22	15 AEF25393	Aef25393 Human mRN
23	22	100.0	22	15 AEF60709	Aef60709 Mouse miR
24	22	100.0	27	14 ADX03789	Adx03789 Human pri
25	22	100.0	30	15 AEF00087	Aef00087 DNA probe
26	22	100.0	40	14 AEB92912	Aeb92912 Human miR
27	22	100.0	70	14 ADX04205	Adx04205 Mouse pri
28	22	100.0	83	12 ADO17089	Ado17089 Human miR
29	22	100.0	83	14 AEB92620	Aeb92620 Human miR
30	22	100.0	83	14 AED35990	Aed35990 Human miR
31	22	100.0	83	15 AEE26703	Aee26703 Hsa miR-1
32	22	100.0	83	15 AEE99350	Aee99350 Human miR
33	22	100.0	83	15 AEE99543	Aee99543 Mouse miR
34	22	100.0	108	14 AEB92619	Aeb92619 Human miR
35	22	100.0	110	14 ADX03045	Adx03045 Human pri
36	22	100.0	110	14 ADX03080	Adx03080 Human pri
37	22	100.0	310	14 ADX03808	Adx03808 Human gen
38	22	100.0	4214	4 AAK72317	Aak72317 Human Imm
39	22	100.0	21	8 ADA00022	Ada00022 D. melano
40	21	95.5	21	14 ADX04045	Adx04045 Human mat
41	21	95.5	21	14 ADX04624	Adx04624 Antisense
42	18.8	85.5	7808	14 ADZ45650	Adz45650 Human pap
43	18.8	85.5	7824	14 ADZ45651	Adz45651 Human pap
44	18	81.8	23	12 ADO17093	Ado17093 Human miR
45	17.8	80.9	21	14 ADX85401	Adx85401 Human/mo

ALIGNMENTS

RESULT 1  
ADA00084  
ADA00084 standard; RNA; 22 BP.  
ID ADA00084;  
AC  
XX  
AC ADA00084;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human miRNA sequence miR-15 SEQ ID NO:81.  
XX  
KW Drosophila melanogaster; human; mouse; microRNA; miRNA; cytosolic;  
KW gene therapy; diagnostic; therapeutic; developmental modulator;  
KW pathogenic modulator; cancer; B-cell chronic leukaemia;  
KW tissue reprogramming; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2003029459-A2.  
XX  
XX PN  
XX 10-APR-2003.  
XX  
XX PD  
XX  
XX PF 27-SEP-2002; 2002WO-EP010861.  
XX  
XX PR 28-SEP-2001; 2001EP-00123453.  
XX  
XX PR 22-MAR-2002; 2002EP-00006712.  
XX  
XX PR 26-JUL-2002; 2002EP-00016772.  
XX  
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG.  
XX  
XX XX  
XX PI Tuschl T, Lagos-Quintana M, Lendeckel W, Meyer J, Rauhut R;  
XX  
XX DR WPL; 2003-381637/36.  
XX  
XX PT New nucleic acid molecule for diagnostic and therapeutic applications and  
XX as a marker or a modulator of developmental or pathogenic processes, e.g.  
XX cancer, comprises microRNAs of a Drosophila melanogaster, a human or a  
XX mouse.  
XX  
XX PS Claim 1; Page 28; 138pp; English.  
XX  
XX CC The present invention describes an isolated nucleic acid molecule (I)

CC comprising a nucleotide sequence of *Drosophila melanogaster*, human or  
CC mouse microRNAs (miRNAs), or their precursors, a complement of it, a  
CC nucleotide sequence that has an affinity of at least 80 % to them or a  
CC nucleotide sequence that hybridises under stringent conditions to them.  
CC Also described: (1) a pharmaceutical composition containing the nucleic  
CC acid and, optionally, a carrier; and (2) identifying mRNA molecules or  
CC precursor molecules, comprising ligating 5' - and 3' -adapter molecules to  
CC the ends of a site/fracti onated RNA population, reverse transcribing the  
CC adapter-containing RNA population and characterising the reverse  
CC transcription products. (1) has cytosolic activity, and can be used in  
CC gene therapy. The pharmaceutical composition is useful for diagnostic and  
CC therapeutic applications, and as a marker or a modulator of developmental  
CC or pathogenic processes, particularly of cancer (e.g., B-cell chronic  
CC leukaemia) or gene expression. The mRNA molecules may also be used in  
CC tissue reprogramming procedures. The present sequence represents an mRNA  
CC sequence from the present invention.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match	100.0%	Score 22;	DB 8;	Length 22;
Best Local Similarity	100.0%	Pred. No. 0.35;		
Matches 22; Conservative	0;	Mismatches	0;	Gaps 0;

Oy		1	VAGCAGCACAAUAUGGUUUGG	22
D8		1	VACAGCACAUUAUGGUUUUGG	22

RESULT 2  
ADA00122

AC ADA00122;

DT 06-NOV-2003 (first entry)

Mouse miRNA sequence mir-15a SEQ ID NO:119.

KW *Drosophila melanogaster*; human; mouse; microRNA; miRNA; cytostatic;

KW pathogenic modulator; cancer; B-cell chronic leukaemia;

KW tissue reprogramming; ss.

OS Mus sp.

PN W02003029459-A2.

PD 10-APR-2003.

PF 27-SEP-2002; 2002WO-EP010881.

PR 28-SEP-2001; 2001EP-00123453.

PR 26-JUL-2002; 2002EP-00016772.

PA (PLAC ) MAX PLANCK GES FOERDERUNG.

PI Tuschl T, Lagos-Quintana M, Lendeckel W, Meyer J, Rauhut R;

DR WPI; 2003-381637/36.

PT New nucleic acid molecule for diagnostic and therapeutic applications and  
PT as a marker or a modulator of developmental or pathogenic processes, e.g.  
PT cancer, comprises microRNAs of a *Drosophila* melanogaster, a human or a  
PT mouse.

PS Claim 1; Page 31; 138pp; English.

CC The present invention describes an isolated nucleic acid molecule (i) CC comprising a nucleotide sequence of *Drosophila melanogaster*, human or CC mouse microRNAs (miRNAs), or their precursors, a complement of it, a CC nucleotide sequence that has an affinity of at least 80 % to them or a CC nucleotide sequence that hybridises under stringent conditions to them.

CC Also described: (1) a pharmaceutical composition containing the nucleic acid and, optionally, a carrier; and (2) identifying miRNA molecules or precursor molecules, comprising ligating 5'- and 3'-adaptor molecules to the ends of a size-fractionated RNA population, reverse transcribing the adaptor-containing RNA population and characterising the reverse transcription products. (1) has cytosstatic activity, and can be used in gene therapy. The pharmaceutical composition is useful for diagnostic and therapeutic applications, and as a marker or a modulator for developmental or pathogenic processes, particularly of cancer (e.g. B-cell chronic leukaemia) or gene expression. The miRNA molecules may also be used in tissue reprogramming procedures. The present sequence represents an miRNA sequence from the present invention.

xx Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

99

Query Match	100.0%	Score 22	DB 8	length 22
Best Local Similarity	100.0%	Pred. No. 0.35		
Matches 22	Conservative 0	Mismatches 0	Indels 0	Gaps 0

<b>QY</b>	1 UAGCAGCACAUAAUGGUGUUG	22
<b>D8</b>	1 UAGCAGCACAUAAUGGUGUUG	22

RESULT 3  
AD017091

ID AD017091 standard; RNA; 22 BP.

AC ADO17091;

DT 12-AUG-2004 (first entry)

Human miR15 processed RNA sequence SeqID3.

KW mir15; mir16; cancer; proliferation; cancer cell; cytostatic; .....

KW chromosome 13q14; human; ss.

OS Homo sapiens.

PN WO2004043387-A2.

PD 27-MAY-2004.

PF 12-NOV-2003; 2003WO-US035777.

PR 13-NOV-2002; 2002US-0425864P.

XX

XX

XX

XX

PT leukemia or prostate cancer, comprises administering to the subject an

XX

XX

CC This invention relates to a novel method of treating an mR15 or mR16  
CC mediated cancer in a subject which comprises administering to the subject  
CC an amount of an isolated mR15 or mR16 gene product such that  
CC proliferation of mR15 or mR16 mediated cancer cells is inhibited. The  
CC mR15 and mR16 micro RNA genes are localised to 13q14 in humans, a  
CC region that is deleted in a significant portion of subjects suffering  
CC from chronic lymphocytic leukaemia or prostate cancer. The products of  
CC the mR15 and mR16 genes have also been found to inhibit the neoplastic  
CC or tumourigenic growth of chronic lymphocytic leukaemia or prostate  
CC cancer cells. The invention may be useful for the production of compounds  
CC with a cytostatic activity. In addition the invention may also be useful  
CC for gene therapy using the mR15 or mR16 gene product. The methods and

CC compositions are useful in diagnosing and treating miR15 or miR16  
CC mediated cancer, i.e. chronic lymphocytic leukemia or prostate cancer.  
CC The present sequence is that of the human miR15 processed RNA sequence  
CC which is used in the method of the invention.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCAUAUGGUGUG 22  
Db 1 UAGCAGCAUAUGGUGUG 22

RESULT 4  
ADP84065  
ID ADP84065 standard; RNA; 22 BP.

AC ADP84065;  
XX 23-SEP-2004 (first entry)

XX Small nucleotide detection-related human miRNA SeqID62.

XX small nucleic acid detection; interfering RNA; detection structure;  
KW miRNA; micro RNA; siRNA; short interfering RNA; human; ss.

XX Homo sapiens.

XX WO2004057017-A2.

XX 08-JUL-2004.

XX 18-DEC-2003; 2003WO-US041549.

XX 18-DEC-2002; 2002US-0434518P.

XX 18-DEC-2003; 2003US-00740256.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Dahlberg JE, Allawi HT, Lyamichev V, Neri BP, Olson-Munoz M;  
PI Chehak L, Olson SM;

XX WPI; 2004-500306/47.

XX Detecting small nucleic acids, such as miRNA and siRNA, by hybridizing an  
PT interfering RNA target to at least one nucleic acid that contains  
PT sequence not complementary to the interfering RNA target to generate a  
PT detection structure.

XX Example 2; SEQ ID NO 62; 97pp; English.

XX This invention relates to a novel method of detecting small nucleic acids  
CC which comprises hybridizing an interfering RNA target to at least one  
CC nucleic acid that contains sequence not complementary to the interfering  
CC RNA target to generate a detection structure, and detecting the detection  
CC structure. The present invention is useful for detecting and  
CC characterizing interfering RNA such as miRNAs (micro RNAs) and siRNAs  
CC (short interfering RNAs), and quantifying interfering RNA expression. The  
CC present sequence is that of an oligonucleotide which was used in the  
CC exemplification of the invention.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCAUAUGGUGUG 22  
Db 1 UAGCAGCAUAUGGUGUG 22

RESULT 5  
ADR83121  
ID ADR83121 standard; RNA; 22 BP.

XX ADR83121;

XX 02-DEC-2004 (first entry)

DE Human miRNA oligo that modulates expression of human target mRNA Seq 23.

XX human; ss; miRNA; microRNA; ontogenesis; cell therapy; cancer;  
KW immune disease; nerve disorder; amyotrophic lateral sclerosis;  
KW Parkinson's disease; Alzheimer's disease; inflammatory disease;  
KW siRNA silencing precursor; cytosolic; immunosuppressive; neurotropic;  
KW neuroprotective; antiinflammatory; immunotherapy.

XX Homo sapiens.

XX WO2004076622-A2.

XX 10-SEP-2004.

XX 10-FEB-2004; 2004WO-JP001433.

XX 10-FEB-2003; 2003US-0445829P.

XX (NNAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX Taira K, Kawasaki H;

XX WPI; 2004-653393/63.

XX Modulating expression of a target gene in a cell, for treating cancer, an  
PT immune disease, or a nerve disorder, comprises introducing into the cell  
PT a polynucleotide that forms a duplex region with an mRNA transcribed from  
PT the target gene.

XX Claim 6; SEQ ID NO 23; 865pp; English.

XX This invention relates to a novel method for modulating the expression of  
CC a target gene in a cell. Specifically, it refers to the introduction into  
CC a cell of a polynucleotide that forms a duplex region with an mRNA  
CC transcribed from the target gene, where the duplex region comprises a  
CC mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that  
CC regulates mRNA at a post-transcriptional level. The present invention  
CC describes a method for controlling ontogenesis of a mammal, function of a  
CC mammalian cell, differentiation of a mammalian cell or viability of a  
CC mammalian cell in the post-transcriptional phase, which comprises  
CC introducing a plasmid vector comprising a promoter and nucleic acid  
CC molecule expressing an miRNA or siRNA silencing precursor to the miRNA.  
CC Accordingly, it provides a cell therapy method for treating cancer,  
CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,  
CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease  
CC by introducing into the cell the miRNA, siRNA silencing precursor to the  
CC miRNA or the plasmid vector. As such, they can be developed into  
CC pharmaceutical compositions that exhibit cytostatic, immunosuppressive,  
CC neurotropic, neuroprotective and antiinflammatory activities and hence can  
CC be used for immunotherapy. This oligonucleotide sequence is a human miRNA  
CC oligo that modulates expression of a target human gene, given in an  
CC exemplification of the invention.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCAUAUGGUGUG 22  
Db 1 UAGCAGCAUAUGGUGUG 22

RESULT 6	
ADXX03284/C	
ID	ADXX03284 standard; DNA; 22 BP.
AC	
XX	
ADXX03284;	
DT	05-MAY-2005 (first entry)
XX	
DE	Antisense oligonucleotide targeting a human miRNA, ISIS27951.
XX	
KW	Antisense oligonucleotide; ss; RNA interference; gene silencing;
KW	Cytostatic; Antidiabetic; Anorectic; Antilipemic; Antiarteriosclerotic;
KW	Hypotensive; Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW	Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW	angiogenesis disorder; cardiovascular disease;
KW	non-insulin dependent diabetes; endocrine disease;
KW	gastrointestinal disease; metabolic disorder; Obesity;
KW	nutritional disorder; hyperlipidemia; atherosclerosis;
KW	hyperension; anorexia nervosa; nutritional disorder;
KW	psychiatric disorder; Alzheimers disease; degeneration;
KW	neurological disease; nervous system injury; neurodegenerative disease;
KW	neurological disorder; 2'-O-methoxyethyl; 2-MOE; phosphorothioate.
XX	
OS	Homo sapiens.
XX	
PN	WO2005013901-A2.
XX	
PD	17-FEB-2005.
XX	
PF	30-JUL-2004; 2004WO-US025300.
XX	
PR	31-JUL-2003; 2003US-0492056P.
PR	31-OCT-2003; 2003US-0516303P.
PR	19-DEC-2003; 2003US-0531596B.
PR	14-APR-2004; 2004US-0562417P.
XX	
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF;
PI	Vickers T, Marcusson EG, Koller E, Swayze EE, Jain R, Bhat B;
PI	Peralta E;
XX	
DR	WPI; 2005-163123/17.
XX	
PT	New oligomeric compound that can hybridize with or sterically interfere
PT	with nucleic acid molecules comprising or encoding small non-coding RNA
PT	targets, useful for treating e.g., cancer and diabetes.
XX	
PS	Example 5; SEQ ID NO 369; 854bp; English.
XX	
CC	The invention relates to an oligomeric compound comprising a first region
CC	and a second region, where at least one region contains a modification,
CC	and a portion of the oligomeric compound is targeted to a small non-
CC	coding RNA target nucleic acid that is miRNA (micro-RNA), or its
CC	precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC	comprising a first oligomeric compound and a second oligomeric compound
CC	(where at least one of the oligomeric compounds contains a modification,
CC	at least a portion of the first oligomeric compound is capable of
CC	hybridizing with at least a portion of the second oligomeric compound,
CC	and at least a portion of the first oligomeric compound is targeted to a
CC	small non-coding RNA target nucleic acid), a pharmaceutical composition
CC	comprising the composition cited above (and a carrier), a kit or assay
CC	device comprising the composition, modulating the expression of a small
CC	non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC	treating or preventing a disease or disorder associated with a small non-
CC	coding RNA target nucleic acid, treating a condition in an animal,
CC	treating or preventing a disease or disorder associated with CD36,
CC	methods of screening an oligomeric compound for an effect on miRNA
CC	signaling, methods of screening a miRNA precursor for an effect in miRNA
CC	signaling, methods of modulating translation (or apoptosis, conversion of
CC	a precursor miRNA into miRNA, or cellular differentiation), identifying
CC	an RNA transcript bound to a small non-coding RNA, arresting (or

CC	delaying) entry of a cell at the G2/M phase, interfering with chromosome segregation, a method of triggering apoptosis, detecting a miRNA precursor, identifying a miRNA target, modulating cellular differentiation, treating a condition associated with adipocyte differentiation in an animal, treating/preventing a disease/disorder associated with aberrant regulation of the cell cycle by miRNAs, maintaining a pluripotent stem cell and identifying a small non-coding RNA binding site. The oligomeric compound is targeted to a region flanking a Drosophila cleavage site within a pri-miRNA. It stimulates an increase in expression of a pri-miRNA. The compounds and compositions are useful for treating a disease or disorder resulting from chromosomal non-cc junction, altered methylation, acetylation, or pseudouridylation state of chromosomes, such as a hyperproliferative condition (e.g., cancer, neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity, Alzheimer's disease, a central nervous system injury or neurodegenerative disorder. The present sequence is an antisense oligonucleotide targeting an miRNA.
CC	
XX	
SO	Sequence 22 BP; 7 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match	100.0%; Score 22; DB 14; Length 22;
Best Local Similarity	68.2%; Pred. No. 0.33;
Matches	15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Oy	1 UAGCAGCACAAUATGCUUGUG 22      ::  ::   ::   ::   ::
Db	22 TAGCAGCACAAUATGCTTGTGG 1
RESULT 7	
ID	ADX03184 standard; RNA; 22 BP.
XX	
AC	ADX03184;
XX	
DT	05-MAY-2005 (first entry)
DE	
XX	Human microRNA (miRNA) mir-15a-l.
XX	
KM	MicronRNA; ds; RNA interference; gene silencing; Cytostatic; Antidiabetic;
KW	Anorectic; Anitlipemic; Antiatherosclerotic; Hypotensive;
KM	Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW	Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW	angiogenesis disorder; cardiovascular disease;
KW	non-insulin dependent diabetes; endocrine disease;
KW	gastrointestinal disease; metabolic disorder; obesity;
KW	nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
KM	hyperemesis; anorexia nervosa; nutritional disorder;
KM	psychiatric disorder; Alzheimers disease; degeneration;
KW	neurological disease; nervous system injury; neurodegenerative disease;
OS	neurological disorder.
XX	
XX	Homo sapiens.
PN	WO2005013901-A2.
XX	
PD	17-FEB-2005.
XX	
PF	30-JUL-2004; 2004WO-US025300.
XX	
PR	31-JUN-2003; 2003US-0492056P.
PR	31-OCT-2003; 2003US-0516303P.
PR	19-DEC-2003; 2003US-0531596P.
PR	14-APR-2004; 2004US-0562417P.
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF,
PI	Vickers T, Marcusson EG, Koller E, Swayze EE, Jain R, Bhat B;
PI	Peralta E;
XX	
DR	WPI; 2005-163123/17.

XX New oligomeric compound that can hybridize with or sterically interfere  
PT with nucleic acid molecules comprising or encoding small non-coding RNA  
PT targets, useful for treating e.g., cancer and diabetes.

PS Example 4; SEQ ID NO 269; 854pp; English.

XX The invention relates to an oligomeric compound comprising a first region  
CC and a second region, where at least one region contains a modification,  
CC and a portion of the oligomeric compound is targeted to a small non-  
CC coding RNA target nucleic acid that is miRNA (micro-RNA), or its  
CC precursor (primary-miRNA, pri-miRNA). Also included are a composition  
CC comprising a first oligomeric compound and a second oligomeric compound  
CC (where at least one of the oligomeric compounds contains a modification,  
CC at least a portion of the first oligomeric compound is capable of  
CC hybridizing with at least a portion of the second oligomeric compound,  
CC and at least a portion of the first oligomeric compound is targeted to a  
CC small non-coding RNA target nucleic acid), a pharmaceutical composition  
CC comprising the composition cited above (and a carrier), a kit or assay  
CC device comprising the composition, modulating the expression of a small  
CC non-coding RNA target nucleic acid in a cell (or tissue or animal),  
CC treating or preventing a disease or disorder associated with a small non-  
CC coding RNA target nucleic acid, treating a condition in an animal,  
CC treating or preventing a disease or disorder associated with C36,  
CC methods of screening an oligomeric compound for an effect on miRNA  
CC signaling, methods of screening a miRNA precursor for an effect in miRNA  
CC signaling, methods of modulating translation (or apoptosis, conversion of  
CC a precursor miRNA into miRNA, or cellular differentiation), identifying  
CC an RNA transcript bound to a small non-coding RNA, arresting (or  
CC delaying) entry of a cell at the G2/M phase, interfering with chromosome  
CC segregation, a method of triggering apoptosis, detecting a miRNA  
CC precursor, identifying a miRNA target, modulating cellular  
CC differentiation, treating a condition associated with adipocyte  
CC differentiation in an animal, treating/preventing a disease/disorder  
CC associated with aberrant regulation of the cell cycle by miRNAs,  
CC maintaining a pluripotent stem cell and identifying a small non-coding  
CC RNA binding site. The oligomeric compound is targeted to a region  
CC flanking a Drosophila cleavage site within a pri-miRNA. It stimulates an  
CC increase in expression of a pri-miRNA. The compounds and compositions are  
CC useful for treating a disease or disorder resulting from chromosomal non-  
CC disjunction, altered methylation, acetylation, or pseudouridylation state  
CC of chromosomes, such as a hyperproliferative condition (e.g., cancer,  
CC neoplasia or angiosarcoma), diabetes (Type 2 diabetes), obesity,  
CC hyperlipidemia, atherosclerosis, arteriosclerosis, hypertension, anorexia,  
CC Alzheimer's disease, a central nervous system injury or neurodegenerative  
CC disorder. The present sequence is a mature miRNA of the invention.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAUGUGUGUG 22  
DB 1 UAGCAGCACAUAUGUGUGUG 22

RESULT 8  
ADY30915  
ID ADY30915 standard; DNA; 22 BP.

XX ADY30915;

XX 05-MAY-2005 (first entry)

XX Micro RNA (miRNA)-related DNA targeted to human E2F3/E1F5A2/FOXAI -SEQ 7.

XX miRNA; micro RNA; RNA interference; gene silencing;

XX E2F transcription factor 3; E2F3;  
XX eukaryotic translation initiation factor 5A2; E1F5A2; forkhead box A1;  
XX FOXAI; hepatocyte nuclear factor 3 alpha; HNF3alpha; ss.

OS Homo sapiens.

XX WO2005017145-A1.

XX 24-FEB-2005.

XX 12-AUG-2004; 2004MO-JP011624.

XX 13-AUG-2003; 2003JP-00293129.

XX (NIBI-) JAPAN BIOLOGICAL INFORMATICS CONSORTIUM.

XX (BITS-) BITS CO LTD.

XX (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX Barrero Roberto Antonio, Tamura T, Imanishi T, Gojobori T;  
XX Taira K, Kawasaki H;  
XX WPI; 2005-196094/20.

XX Identifying a gene under regulation of functional RNA, involves setting  
PT ambiguity of different standards in conserved and unconserved region of  
PT functional RNA, searching for gene which is complementary to functional  
PT RNA.

PS Claim 8; SEQ ID NO 7; 38pp; Japanese.

XX The invention relates to a novel method for identifying or presuming a  
CC functional miRNA (micro RNA) molecule of base length of 16-25 and a gene  
CC which is regulated as a result of targeting by the miRNA. The method  
CC comprises determining and classifying the base sequences of functional  
CC RNA molecules into conserved and unconserved regions, setting ambiguities  
CC of different standards in these regions and searching for a candidate  
CC gene which has a base sequence complementary to the functional RNA  
CC molecule. The method of the invention may be useful for identifying a  
CC gene whose expression is under regulation by a functional RNA molecule of  
CC base length of 16-25. The method is thus useful for developing treatments  
CC for a disease or for treating a disease by controlling the biological  
CC function of the target gene. The current sequence is that of a micro RNA  
CC (miRNA)-related DNA of the invention which is targeted to a human gene.  
CC Specifically, human E2F transcription factor 3 (E2F3), eukaryotic  
CC translation initiation factor 5A2 (E1F5A2) and forkhead box A1 (FOXAI,  
CC hepatocyte nuclear factor 3 alpha, HNF3alpha) are referred to in claim 9.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 22;  
Best Local Similarity 68.2%; Pred. No. 0.35;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAUGUGUGUG 22  
DB 1 TAGCAGCACAUAUGUGUGUG 22

RESULT 9  
ADX85423  
ID ADX85423 standard; RNA; 22 BP.

XX ADX85423;

XX 05-MAY-2005 (first entry)

XX Human/mouse miR-15 microRNA that binds hOMP1 target mRNA.

XX microRNA recognition element; MRE; bioinformatics; gene expression; ss.

XX Homo sapiens.

XX Mus sp.

XX Key Location/Qualifiers

FT misc\_binding 1..17  
FT /\*tag= a  
FT /bound\_molecly= "hOMP1 MRE"

```
FT /note= "Forms double stranded region with nucleotides 17-
FT 1"
XX
XX MO2005017111-A2.
XX
XX 24-FEB-2005.
XX
XX 15-JUL-2004; 2004WO-US022934.
XX
XX 15-JUL-2003; 2003US-0487321P.
XX
XX (UTYPE-) UNIV PENNSYLVANIA.
XX
XX Hatziogeorgiou AG, Mourelatos Z;
XX
XX WPI; 2005-182352/19.
XX
XX Identifying a microRNA-recognition element by comparing the degree of
XX complementarity of a microRNA nucleotide sequence to an mRNA sequence.
XX
XX Example 1; Fig 6; 51pp; English.
XX
XX This invention relates to a novel method for identifying a microRNA-
XX recognition element (MRE). Specifically, it refers to comparing the
XX degree of complementarity of a microRNA nucleotide sequence (miRNA) to an
XX mRNA target sequence in order to identify the presence of a sequence that
XX is indicative of an MRE for the microRNA. In particular, it refers to
XX miRNA-MRE recognition rules that allow prediction of human and mouse
XX miRNA targets. The present invention also describes determining the free
XX energy of the microRNA bound to the selected 3' untranslated region of an
XX mRNA sequence i.e. the MRE sequence. Furthermore, it provides an
XX oligonucleotide that is synthesized having the sequence of the generated
XX microRNA and contacting the microRNA with a cell expressing the mRNA in
XX order to down regulate expression of that mRNA. It describes a system for
XX identifying a microRNA-recognition element as comprising an interface for
XX inputting mRNA sequences, a database of mRNA sequences or a link for
XX connecting to a remote data input interface, data or a database of mRNA
XX sequences, and a processor with instructions for comparing mRNA sequences
XX to microRNA sequences to identify an MRE. This oligonucleotide is a
XX human/ mouse microRNA sequence that binds to a microRNA-recognition
XX element of the target mRNA given in an exemplification of the invention.
XX
XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 14; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 0.35;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 UAGCAGCACAUAAUGGUTUGUG 22
XX |||||
XX 1 UAGCAGCACAUAAUGGUTUGUG 22
XX
XX Db
XX
XX RESULT 10
XX ADZ20390
XX ID ADZ20390 standard; RNA; 22 BP.
XX
XX AC ADZ20390;
XX
XX DT 16-JUN-2005 (first entry)
XX
XX DE Human hematopoietic miRNA, miR-15a Bl_F06-2, SEQ ID NO: 9 #2.
XX
XX KW Expression; gene therapy; hematological disease; cancer; infection;
XX cytostatic; antibacterial; virucide; fungicide; antimicrobial; neoplasm;
XX ss; micro RNA; miRNA.
XX
XX OS Homo sapiens.
XX
XX PN US2005075492-A1.
XX
XX PD 07-APR-2005.
XX
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PF 06-AUG-2004; 2004US-00913288.
XX
XX 07-AUG-2003; 2003US-0493239P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Chen C, Bartel D, Lodish H;
XX
XX WPI; 2005-283812/29.
XX
XX DR
XX
XX PT New precursor microRNA molecule comprises isolated nucleic acid
XX comprising a stem-loop structure and a microRNA flanking sequence, useful
XX for treating hematopoietic disorders including cancers, viral, bacterial,
XX or fungal infections.
XX
XX PS Disclosure; SEQ ID NO 9; 39pp; English.
XX
XX CC The present invention relates to a precursor microRNA (miRNA) molecule
XX comprising a stem-loop structure and a microRNA flanking sequence. The
XX invention also provides a method for producing miRNA. The invention is
XX useful for treating hematopoietic disorders including cancers, e.g.
XX leukemia, lymphoma, bladder cancer, brain cancer, head and neck cancer,
XX prostate cancer, or rectal cancer and infections, e.g. viral, bacterial,
XX or fungal infections. The precursor miRNA is useful for regulating the
XX expression of protein-coding genes at the posttranscriptional level and
XX also be used as therapeutics and as research tools, e.g. analyzing gene
XX function. The invention is useful in gene therapy. The present sequence
XX is the human hematopoietic miRNA plays a role in hematopoiesis. The
XX current sequence is that of the human miRNA which is located on
XX chromosome 13q13.3. Note: The present sequence is the SEQ ID NO: 9 which
XX is shown on page 7. This sequence differs from the SEQ ID NO: 9 given in
XX the sequence listing (see ADZ20370).
XX
XX SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 14; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 0.35;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 UAGCAGCACAUAAUGGUTUGUG 22
XX |||||
XX 1 UAGCAGCACAUAAUGGUTUGUG 22
XX
XX Db
XX
XX RESULT 11
XX AEC36205
XX ID AEC36205 standard; RNA; 22 BP.
XX
XX AC AEC36205;
XX
XX DT 03-NOV-2005 (first entry)
XX
XX DE Nucleotide sequence of known human miRNA #9.
XX
XX KW RNA interference; gene silencing; microRNA; miRNA; gene therapy;
XX Huntingtons chorea; cardiovascular disease; cardiovascular gen.;
XX immune disorder; immunomodulator; liver disease; hepatotropic;
XX gastrointestinal disease; viral infection; virucide; infection; pain;
XX analgesic; neurological disease; metabolic disorder; metabolic;
XX metabolic disorder; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2005078096-A2.
XX
XX PD 25-AUG-2005.
XX
XX PF 09-FEB-2005; 2005WO-US004206.
XX
XX PR 09-FEB-2004; 2004US-0543467P.
XX
XX PA (UTMA-) UNIV MASSACHUSETTS.
XX
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PI Zamore PD, Aronin N, Broderick J;  
XX WPI; 2005-571602/58.  
XX  
PT New RNA-silencing agent comprising an mRNA targeting moiety, a linking  
PT moiety, and a miRNA recruiting moiety, useful for repressing translation  
PT of a target mRNA for treating Huntington's disease.  
XX  
XX Disclosure; Page 11; 80pp; English.  
XX  
CC The specification describes a RNA-silencing agent, comprising an mRNA  
CC targeting moiety, a linking moiety, and a microRNA (miRNA) recruiting  
CC moiety. The RNA-silencing agent of the invention is useful for the  
CC manufacture of medicament for repressing mutant gene expression, such as  
CC repressing translation of a target mRNA. It is useful for treating  
CC Huntington's disease in this manner. The agent may also be useful in the  
CC treatment of one or more of cellular proliferative and/or differentiative  
CC disorders, cardiovascular disorders, immune disorders, hematopoietic  
CC disorders, liver disorders, viral diseases, pain or metabolic disorders.  
CC AEC36197-AEC36300 represent known human miRNAs.  
XX  
SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;  
Query Match 100.0%; Score 22; DB 14; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 UAGCAGCACAUAUGGUUGUG 22  
1 UAGCAGCACAUAUGGUUGUG 22  
DB  
RESULT 12  
AED35921 ID AED35921 standard; DNA; 22 BP.  
AC AED35921;  
XX  
DT 15-DEC-2005 (first entry)  
XX  
DE Hsa-miR-15a DNA target.  
XX  
KM RNA interference; RNA purification; RNA amplification; gene silencing;  
KM RNA detection; micro RNA; miRNA; miR-15a; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 22 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= 3' phosphorylated"  
XX  
PN WO2005098029-A2.  
XX  
PD 20-OCT-2005.  
XX  
PF 07-APR-2005; 2005WO-DK000239.  
XX  
XX 07-APR-2004; 2004DK-00000578.  
XX 23-JUL-2004; 2004DK-00001146.  
XX 11-AUG-2004; 2004DK-00001218.  
XX 15-OCT-2004; 2004DK-00001587.  
XX 28-JAN-2005; 2005DK-00000140.  
XX  
XX (EXIQ-) EXIQON AS.  
XX  
PI Jacobsen N, Kongsbak L, Kauppinen S, Echwald SM, Mouritzen P;  
PI Nielsen PS, Norholm M;  
XX  
XX WPI; 2005-714540/73.  
XX  
PT Isolating, purifying, amplifying, detecting, identifying, quantifying or

PT capturing non-coding RNAs such as micro RNA or small interfering RNA  
PT (siRNA), involves using oligonucleotide containing nucleoside analogs.  
XX  
XX Example; Page 69; 180pp; English.  
XX  
CC The present invention relates to the use of an oligonucleotide for the  
CC isolation, purification, amplification, detection, identification,  
CC quantification or capture of microRNA (miRNA) or small interfering RNA  
CC (siRNA), where the oligonucleotide contains a number of nucleoside  
CC analogs. The method uses 2 anchored tagging probes, each designed in  
CC combination to detect a complementary target sequence, e.g. a short RNA  
CC sequence, where the first tagging probe hybridizes to a first region  
CC within a target sequence and the second tagging probe hybridizes to a  
CC second region within the same complementary target sequence, e.g. a short  
CC RNA target sequence that is adjacent to the first region. In a preferred  
CC mode, one of the tagging probes is 5' phosphorylated to enable covalent  
CC coupling of the 2 contiguous tagging probes hybridized to the  
CC complementary target sequence by a ligase to form a single  
CC oligonucleotide sequence. The method takes advantage of substitution of  
CC the recognition sequences with high-affinity nucleotide analogs, e.g.  
CC locked nucleic acid (LNA), for sensitive and specific hybridization to  
CC short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is  
CC followed by real-time quantitative PCR (qPCR) of the target sequence,  
CC e.g. ribonucleic acid-templated, covalently joined oligonucleotide  
CC molecules using anchor sequences attached to the tagging probes as  
CC priming sites for the PCR primers and a short detection probe with  
CC sufficient duplex stability to allow binding to the amplicon, and  
CC employing any of a variety of detection principles used in homogeneous  
CC assays. In the preferred mode, the detection probe is substituted with  
CC duplex-stabilizing, high-affinity nucleotide analogs, e.g. LNA, and  
CC preferably oxy-LNA, to allow the use of short detection probes in the  
CC real-time qPCR. The method is useful for detecting and quantifying  
CC individual small RNA molecules in complex mixtures of different nucleic  
CC acids, and for detecting, testing, diagnosing or quantifying miRNAs,  
CC siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative mRNA  
CC splice variants implicated in, or connected to, human disease in complex  
CC nucleic acid samples, e.g. from cancer patients. The present sequence is  
CC that of hsa-miR-15a DNA, which was used as a target sequence in a real-  
CC time qPCR assay of human miR-15a in an example from the invention.  
XX  
SQ Sequence 22 BP; 6 A; 3 C; 6 G; 7 T; 0 U; 0 Other;  
Query Match 100.0%; Score 22; DB 14; Length 22;  
Best Local Similarity 68.2%; Pred. No. 0.35;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
OY 1 UAGCAGCACAUAUGGUUGUG 22  
1 UAGCAGCACAUAUGGUUGUG 22  
DB  
RESULT 13  
AED35925 ID AED35925 standard; RNA; 22 BP.  
AC AED35925;  
XX  
DT 15-DEC-2005 (first entry)  
XX  
DE Hsa-miR-15a RNA target.  
XX  
KM RNA interference; RNA purification; RNA amplification; gene silencing;  
KM RNA detection; micro RNA; miRNA; miR-15a; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2005098029-A2.  
XX  
PN 20-OCT-2005.  
XX  
PD 07-APR-2005; 2005WO-DK000239.  
XX  
PF 07-APR-2004; 2004DK-00000578.  
XX  
PR

PR 23-JUL-2004; 2004DK-00001146.  
PR 11-AUG-2004; 2004DK-00001218.  
PR 15-OCT-2004; 2004DK-00001587.  
PR 28-JAN-2005; 2005DK-00000140.  
XX  
XX (EXIQ-) EXIQON AS.  
XX  
PI Jacobsen N, Kongsbak L, Kaupinen S, Echwald SM, Mouritzen P;  
PI Nielsen PS, Norholm M;  
XX  
XX WPI; 2005-714540/73.  
XX  
XX Isolating, purifying, amplifying, detecting, identifying, quantifying or  
PT capturing non-coding RNAs such as micro RNA or small interfering RNA  
PT (siRNA), involves using oligonucleotide containing nucleoside analogs.  
XX  
XX Example; Page 69; 180pp; English.  
XX  
XX The present invention relates to the use of an oligonucleotide for the  
CC isolation, purification, amplification, detection, identification,  
CC quantification or capture of microRNA (miRNA) or small interfering RNA  
CC (siRNA), where the oligonucleotide contains a number of nucleoside  
CC analogs. The method uses 2 anchored tagging probes, each designed in  
CC combination to detect a complementary target sequence, e.g. a short RNA  
CC sequence, where the first tagging probe hybridizes to a first region  
CC within a target sequence and the second tagging probe hybridizes to a  
CC second region within the same complementary target sequence, e.g. a short  
CC RNA target sequence that is adjacent to the first region. In a preferred  
CC mode, one of the tagging probes is 5' phosphorylated to enable covalent  
CC coupling of the 2 contiguous tagging probes hybridized to the  
CC complementary target sequence by a ligase to form a single  
CC oligonucleotide sequence. The method takes advantage of substitution of  
CC the recognition sequences with high-affinity nucleotide analogs, e.g.  
CC locked nucleic acid (LNA), for sensitive and specific hybridization to  
CC short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is  
CC followed by real-time quantitative PCR (qPCR) of the target sequence,  
CC e.g. ribonucleic acid-templated, covalently joined oligonucleotide  
CC molecules using anchor sequences attached to the tagging probes as  
CC priming sites for the PCR primers and a short detection probe with  
CC sufficient duplex stability to allow binding to the amplicon, and  
CC employing any of a variety of detection principles used in homogeneous  
CC assays. In the preferred mode, the detection probe is substituted with  
CC duplex-stabilizing, high-affinity nucleotide analogs, e.g. LNA, and  
CC preferably oxy-LNA, to allow the use of short detection probes in the  
CC real-time qPCR. The method is useful for detecting and quantifying  
CC individual small RNA molecules in complex mixtures of different nucleic  
CC acids, and for detecting, testing, diagnosing or quantifying miRNAs, mRNA  
CC siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative  
CC splice variants implicated in, or connected to, human disease in complex  
CC nucleic acid samples, e.g. from cancer patients. The present sequence is  
CC that of hsa-miR-15a RNA, which was used as a target sequence in a real-  
CC time qPCR assay of human miR-15a in an example from the invention.  
XX  
XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;  
SQ  
Query Match 100.0%; Score 22; DB 14; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 UAGCAGCACAUAAUGGUTUGUG 22  
DB 1 UAGCAGCACAUAAUGGUTUGUG 22  
RESULT 14  
AED35991  
ID AED35991 standard; RNA; 22 BP.  
XX  
XX AED35991;  
AC  
XX 15-DEC-2005 (first entry)  
DT  
XX Human micro RNA miR-15a.  
DE

XX  
XX RNA interference; RNA purification; RNA amplification; gene silencing;  
XX RNA detection; micro RNA; miRNA; miR-15a; ss.  
XX  
XX Homo sapiens.  
XX  
XX W02005098029-A2.  
XX  
XX  
XX 20-OCT-2005.  
XX  
XX 07-APR-2005; 2005WO-DK000239.  
XX  
XX  
XX 07-APR-2004; 2004DK-00000578.  
XX 23-JUL-2004; 2004DK-00001146.  
XX 11-AUG-2004; 2004DK-00001218.  
XX 15-OCT-2004; 2004DK-00001587.  
XX 28-JAN-2005; 2005DK-00000140.  
XX  
XX (EXIQ-) EXIQON AS.  
XX  
XX Jacobsen N, Kongsbak L, Kaupinen S, Echwald SM, Mouritzen P;  
XX PI Nielsen PS, Norholm M;  
XX  
XX WPI; 2005-714540/73.  
XX  
XX Isolating, purifying, amplifying, detecting, identifying, quantifying or  
PT capturing non-coding RNAs such as micro RNA or small interfering RNA  
PT (siRNA), involves using oligonucleotide containing nucleoside analogs.  
XX  
XX Disclosure; Fig 29; 180pp; English.  
XX  
XX The present invention relates to the use of an oligonucleotide for the  
CC isolation, purification, amplification, detection, identification,  
CC quantification or capture of microRNA (miRNA) or small interfering RNA  
CC (siRNA), where the oligonucleotide contains a number of nucleoside  
CC analogs. The method uses 2 anchored tagging probes, each designed in  
CC combination to detect a complementary target sequence, e.g. a short RNA  
CC sequence, where the first tagging probe hybridizes to a first region  
CC within a target sequence and the second tagging probe hybridizes to a  
CC second region within the same complementary target sequence, e.g. a short  
CC RNA target sequence that is adjacent to the first region. In a preferred  
CC mode, one of the tagging probes is 5' phosphorylated to enable covalent  
CC coupling of the 2 contiguous tagging probes hybridized to the  
CC complementary target sequence by a ligase to form a single  
CC oligonucleotide sequence. The method takes advantage of substitution of  
CC the recognition sequences with high-affinity nucleotide analogs, e.g.  
CC locked nucleic acid (LNA), for sensitive and specific hybridization to  
CC short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is  
CC followed by real-time quantitative PCR (qPCR) of the target sequence,  
CC e.g. ribonucleic acid-templated, covalently joined oligonucleotide  
CC molecules using anchor sequences attached to the tagging probes as  
CC priming sites for the PCR primers and a short detection probe with  
CC sufficient duplex stability to allow binding to the amplicon, and  
CC employing any of a variety of detection principles used in homogeneous  
CC assays. In the preferred mode, the detection probe is substituted with  
CC duplex-stabilizing, high-affinity nucleotide analogs, e.g. LNA, and  
CC preferably oxy-LNA, to allow the use of short detection probes in the  
CC real-time qPCR. The method is useful for detecting and quantifying  
CC individual small RNA molecules in complex mixtures of different nucleic  
CC acids, and for detecting, testing, diagnosing or quantifying miRNAs,  
CC siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative  
CC splice variants implicated in, or connected to, human disease in complex  
CC nucleic acid samples, e.g. from cancer patients. The present sequence is  
CC that of human miRNA Hsa miR-15a, which was used as the target in examples  
CC from the invention.  
XX  
XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;  
SQ  
Query Match 100.0%; Score 22; DB 14; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 UAGCAGCACAUAAUGGUTUGUG 22



Db 1 UAGCAGCACAUAAUGGUGUG 22

RESULT 15

AED53385  
ID AED53385 standard; RNA; 22 BP.

AC AED53385;

DT 29-DEC-2005 (first entry)

DE Human target / micro RNA oligo, hsa-mir-15.

KW RNA interference; micro RNA; miRNA; transcription; gene regulation;  
microarray; ss.

OS Homo sapiens.

PN JP2005296014-A.

PD 27-OCT-2005.

PF 06-APR-2005; 2005JP-00109915.

PR 06-APR-2004; 2004US-00818956.

PA (EPPE-) EPENDORF ARRAY TECHNOLOGIES SA.

PI Van Velfer C, Lemacre J, Bulov S, Samathoe N;

DR WPI; 2005-753146/77.

PT Determining RNA interference mediated transcriptional regulation of cell,  
by ligating micro RNA of cell to polynucleotide by which target was  
labeled and hybridizing it to probe for transcription material, in array,  
detecting signal.

PS Claim 31; Page 20; 30pp; Japanese.

CC The invention relates to a novel method for determining RNA interference  
(RNAi) mediated transcriptional regulation of a cell, by determining  
patterns of at least 3 micro RNAs (miRNAs). The method involves preparing  
an array with a capture probe of transcription material from the DNA of a  
cell, isolating an miRNA pool existing latently from the cell, extending  
the miRNA or ligating it to a polynucleotide with a labeled target.  
CC hybridizing the polynucleotide with a probe in an array and detecting a  
signal from the array. The invention further includes a kit for carrying  
out the above method. The method is useful for determining RNAi mediated  
transcriptional regulation of a cell. This sequence represents a human  
target / miRNA oligo for use in a microarray of the invention.

SO Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.35;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUGGUGUG 22

Db 1 UAGCAGCACAUAAUGGUGUG 22

Search completed: November 1, 2006, 22:24:57  
Job time : 107.39 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 20:59:58 ; Search time 38.1333 Seconds  
(without alignments)  
1079.486 Million cell updates/sec

Title: US-10-706-798-3  
Sequence: 1 uagcagcacaauagguugug 22

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: Issued Patents\_NA.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1.COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5.COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A.COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7.COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H.COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP.COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE.COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/Backfile1.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/Backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	17.2	78.2	601 3	US-09-949-016-76948 A Sequence 76948, A
2	17.2	78.2	117807 3	US-09-949-016-15525 A Sequence 15525, A
3	17.2	78.2	189560 3	US-09-949-016-17202 A Sequence 17202, A
4	17.2	78.2	235341 3	US-09-949-016-13978 A Sequence 13978, A
5	16.8	76.4	601 3	US-09-949-016-110759 A Sequence 110759, A
6	16.8	76.4	601 3	US-09-949-016-110920 A Sequence 110920, A
7	16.8	76.4	601 3	US-09-949-016-111081 A Sequence 111081, A
8	16.8	76.4	601 3	US-09-949-016-111242 A Sequence 111242, A
9	16.8	76.4	966 3	US-09-248-796A-5921 A Sequence 5921, A
10	16.8	76.4	2319 3	US-09-070-356-1 A Sequence 1, Appl1
11	16.8	76.4	2334 2	US-08-406-070-1 A Sequence 1, Appl1
12	16.8	76.4	43991 5	US-09-949-016-252 A Sequence 252, App
13	16.8	76.4	174170 3	US-09-949-016-14810 A Sequence 14810, A
14	16.8	76.4	174170 3	US-09-949-016-14811 A Sequence 14811, A
15	16.8	76.4	174318 3	US-09-949-016-11880 A Sequence 11880, A
16	16.8	76.4	174318 3	US-09-949-016-14812 A Sequence 14812, A
17	16.8	76.4	174318 3	US-09-949-016-14813 A Sequence 14813, A
18	16.6	75.5	601 3	US-09-949-016-17630 A Sequence 17630, A
19	16.6	75.5	601 3	US-09-949-016-36194 A Sequence 36194, A
20	16.6	75.5	601 3	US-09-949-016-54602 A Sequence 54602, A
21	16.6	75.5	601 3	US-09-949-016-54634 A Sequence 54634, A
22	16.6	75.5	601 3	US-09-949-016-54666 A Sequence 54666, A
23	16.6	75.5	601 3	US-09-949-016-119031 A Sequence 119031, A

24	16.6	75.5	601 3	US-09-949-016-119067 A Sequence 119067, A
25	16.6	75.5	601 3	US-09-949-016-119103 A Sequence 119103, A
26	16.6	75.5	601 3	US-09-949-016-119139 A Sequence 119139, A
27	16.6	75.5	601 3	US-09-949-016-119175 A Sequence 119175, A
28	16.6	75.5	601 3	US-09-949-016-119211 A Sequence 119211, A
29	16.4	74.5	1365 3	US-09-949-016-2063 A Sequence 2063, A
30	16.4	74.5	6946 3	US-09-949-016-13805 A Sequence 13805, A
31	16.2	73.6	601 3	US-09-949-016-46039 A Sequence 46039, A
32	16.2	73.6	601 3	US-09-949-016-92412 A Sequence 92412, A
33	16.2	73.6	601 3	US-09-949-016-137903 A Sequence 137903, A
34	16.2	73.6	777 3	US-08-956-171B-1156 A Sequence 1156, A
35	16.2	73.6	777 3	US-08-781-986A-1156 A Sequence 1156, A
36	16.2	73.6	1140 3	US-08-248-796A-4772 A Sequence 4772, A
37	16.2	73.6	1671 3	US-09-248-796A-4660 A Sequence 4660, A
38	16.2	73.6	4880 3	US-09-402-929-5 A Sequence 5, Appl1
39	16.2	73.6	7868 10	US-09-676-519-19. A Sequence 19, Appl1
40	16.2	73.6	43576 3	US-09-949-016-12224 A Sequence 12224, A
41	16.2	73.6	52711 3	US-09-949-016-15618 A Sequence 15618, A
42	16.2	73.6	52865 3	US-09-949-016-16267 A Sequence 16267, A
43	16.2	73.6	54531 3	US-09-949-016-14385 A Sequence 14385, A
44	16.2	73.6	72602 3	US-09-949-016-13058 A Sequence 13058, A
45	16.2	73.6	103712 3	US-09-949-016-13058 A Sequence 13058, A

# ALIGNMENTS

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RESULT 1
US-09-949-016-76948
; Sequence 76948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76948
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-76948

Query Match      78.2% Score 17.2; DB 3; Length 601;
Best Local Similarity 59.1% Pred. No. 72;
Matches 1; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Oy      1 uagcagcacaauagguugug 22
Db      169 TAGAGCACAATAATGTTTGTG 190

RESULT 2
US-09-949-016-15525
; Sequence 15525, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 15525
/ LENGTH: 117807
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-15525
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Query Match      78.2%; Score 17.2; DB 3; Length 117807;
Best Local Similarity 59.1%; Pred. No. 1.5e+02;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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OY      1 UAGCAGCACAAUAGUGUUG 22
      :||| ||| ||| ||| ||| :|||
Db      29126 TAGCATCATATATATGCTGTG 29147
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RESULT 3
US-09-949-016-17202
/ Sequence 17202, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 17202
/ LENGTH: 189560
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(189560)
/ OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17202
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Query Match      78.2%; Score 17.2; DB 3; Length 189560;
Best Local Similarity 59.1%; Pred. No. 1.6e+02;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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```
OY      1 UAGCAGCACAAUAGUGUUG 22
      :||| ||| ||| ||| ||| :|||
Db      130962 TAGCTGACATATATGCTGTG 130983
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RESULT 4
US-09-949-016-13978/c
/ Sequence 13978, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
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/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 13978
/ LENGTH: 236341
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(236341)
/ OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13978
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Query Match      78.2%; Score 17.2; DB 3; Length 236341;
Best Local Similarity 59.1%; Pred. No. 1.7e+02;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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```
OY      1 UAGCAGCACAAUAGUGUUG 22
      :||| ||| ||| ||| ||| :|||
Db      187064 TAGAGGCAAAATGCTTGTG 187043
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RESULT 5
US-09-949-016-110759
/ Sequence 110759, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 110759
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-110759
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Query Match      76.4%; Score 16.8; DB 3; Length 601;
Best Local Similarity 65.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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```
OY      1 UAGCAGCACAAUAGUGUUG 20
      :||| ||| ||| ||| ||| :|||
Db      398 TAGCAGCACATATATGCTATG 417
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```
RESULT 6
US-09-949-016-110920
/ Sequence 110920, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110920
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-110920

Query Match          76.4%; Score 16.8; DB 3; Length 601;
Best Local Similarity 65.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy      1 UAGCAGCACAUAAUGUUUG 20
Db      398 TAGCAGCACATATGCTATG 417

RESULT 7
US-09-949-016-111081
; Sequence 111081, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111081
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-111081

Query Match          76.4%; Score 16.8; DB 3; Length 601;
Best Local Similarity 65.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy      1 UAGCAGCACAUAAUGUUUG 20
Db      398 TAGCAGCACATATGCTATG 417

RESULT 8
US-09-949-016-111242
; Sequence 111242, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 111242
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-111242

Query Match          76.4%; Score 16.8; DB 3; Length 601;
Best Local Similarity 65.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy      1 UAGCAGCACAUAAUGUUUG 20
Db      398 TAGCAGCACATATGCTATG 417

RESULT 9
US-09-248-796A-5921/C
; Sequence 5921, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5921
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5921

Query Match          76.4%; Score 16.8; DB 3; Length 966;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy      3 GCAGCAGCAUAAUGUUUG 22
Db      734 GCAGCAATATATGTTGTG 715

RESULT 10
US-09-070-356-1/C
; Sequence 1, Application US/09070356
; Patent No. 6228631
; GENERAL INFORMATION:
; APPLICANT: Alex Zhu
; APPLICANT: Jack Goldstein
; TITLE OF INVENTION: Recombinant a-N-
; TITLE OF INVENTION: Acetylglucosaminidase
; TITLE OF INVENTION: Enzyme and cDNA Encoding
; TITLE OF INVENTION: Said Enzyme
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amster, Rothstein & Edenstein
; STREET: 90 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,356
; FILING DATE:
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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/037,248
/ FILING DATE: March 26, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pasqualini, Patricia A.
/ REGISTRATION NUMBER: 34,894
/ REFERENCE/DOCKET NUMBER: 63475/12
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 697-5995
/ TELEFAX: (212) 266-0854 or 266-0082
/ TELETYPE: TWX 710-581-4766
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2319
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE:
/ DESCRIPTION: cDNA to mRNA
/ HYPOTHEICAL: no
/ ANTI-SENSE: yes
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM: chicken liver
/ STRAIN:
/ INDIVIDUAL ISOLATE:
/ DEVELOPMENTAL STAGE:
/ HAPLOTYPE:
/ TISSUE TYPE:
/ CELL TYPE:
/ ORGANELLE:
/ IMMEDIATE SOURCE: library
/ POSITION IN GENOME: unknown
/ CHROMOSOME/SEGMENT:
/ MAP POSITION:
/ UNITS:
/ FEATURE:
/ NAME/KEY: chicken liver a-N-
/ NAME/KEY: acetylglucosaminidase
/ LOCATION:
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION:
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ TITLE:
/ JOURNAL:
/ VOLUME:
/ PAGES:
/ DATE:
/ DOCUMENT NUMBER:
/ FILING DATE:
/ PUBLICATION DATE:
/ RELEVANT RESIDUES IN SEQ ID NO:
/ US-09-070-356-1
/
/ Query Match 76.4%; Score 16.8; DB 3; Length 2319;
/ Best Local Similarity 60.0%; Pred. No. 1.4e+02;
/ Matches 12; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
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/ QY 3 GCAGCACUAUAGUGUUGUG 22
/ Db 673 GCAGCACATCCTCGTTTGTG 654
/
/ RESULT 11
/ US-08-406-070-1/c
/ Sequence 1, Application US/08406070
/ Patent No. 5610063
/ GENERAL INFORMATION:
/ APPLICANT: Smith, Daniel S.
/ APPLICANT: Walker, John C.
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/ TITLE OF INVENTION: A cDNA For
/ TITLE OF INVENTION: alpha-N-acetyl-galactosaminidase From Gallus domesticus
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Reising, Ethelington, Barnard, Perry & Milton
/ STREET: P.O. Box 4390
/ CITY: Troy
/ STATE: Michigan
/ COUNTRY: US
/ ZIP: 48099
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/406,070
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kohn, Kenneth I.
/ REGISTRATION NUMBER: 30,955
/ REFERENCE/DOCKET NUMBER: UMO P-317
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (610) 689-3500
/ TELEFAX: (610) 689-4071
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2334 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 2316..2334
/ US-08-406-070-1
/
/ Query Match 76.4%; Score 16.8; DB 2; Length 2334;
/ Best Local Similarity 60.0%; Pred. No. 1.4e+02;
/ Matches 12; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
/
/ QY 3 GCAGCACUAUAGUGUUGUG 22
/ Db 670 GCAGCACATCCTCGTTTGTG 651
/
/ RESULT 12
/ US-09-984-429-252
/ Sequence 252, Application US/09984429
/ Patent No. 7026447
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 53 Human Secreted Proteins
/ FILE REFERENCE: P2018P2
/ CURRENT APPLICATION NUMBER: US/09/984,429
/ CURRENT FILING DATE: 2001-10-30
/ PRIOR APPLICATION NUMBER: 60/244,591
/ PRIOR FILING DATE: 2000-11-01
/ PRIOR APPLICATION NUMBER: 09/288,143
/ PRIOR FILING DATE: 1999-04-08
/ PRIOR APPLICATION NUMBER: PCT/US98/21142
/ PRIOR FILING DATE: 1998-10-08
/ PRIOR APPLICATION NUMBER: 60/061,463
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/061,529
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/071,498
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/061,527
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/061,536
/ PRIOR FILING DATE: 1997-10-09
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1  PRIOR APPLICATION NUMBER: 60/061,532
2  PRIOR FILING DATE: 1997-10-09
3  NUMBER OF SEQ ID NOS: 727
4  SOFTWARE: PatentIn Ver. 2.0
5  SEQ ID NO 252
6  LENGTH: 43991
7  TYPE: DNA
8  ORGANISM: Homo sapiens
9  US-09-384-429--252

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Query Match	76.4%	Score 16.8;	DB 5;	Length 43991;
Best Local Similarity	65.0%;	Pred. No. 2.1e+02;		
Matches 13; Conservative	5;	Mismatches 2;	Indels 0;	Gaps 0;

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QY      1 UAGCAGCACAUAUGGUG 20
      : ||||| ||| :|:::|
Db     10240 TAGCAGACACAATGGTTG 10259

```

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RESULT 13
US-09-949-016-14810
; Sequence 14810, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14810
; LENGTH: 174170
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174170)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14810

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Query Match	76.4%;	Score 16.8;	DB 3;	Length 174170;
Best Local Similarity	65.0%;	Pred. No. 2.5e+02;		
Matches 13;	Conservative 5;	Mismatches 2;	Indels 0;	Gaps 0;

```

Oy      1 UAGCAGCACAUAAGUGUUUG 20
          :|:|:|:|:|:|:|:|:|:|
Db      56372 TAGCAGCACAATAATGCTATG 56391

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RESULT 14
US-09-949-016-14811
; Sequence 14811, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

```

```

? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 14811
? LENGTH: 174170
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1) ... (174170)
? OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14811

```

Query Match	76.4%;	Score 16.8;	DB 3;	length 174170;
Best Local Similarity	65.0%;	Pred. No. 2.5e+02;		
Matches 13;	Conservative 5;	Mismatches 2;	Indels 0;	Gaps 0;

```
QY      1 UAGCAGCACUAUUGGUTUG 20  
       :|||||||::|::|  
Db     56372 TAGCAGCATATGTCTATG 56391
```

```

RESULT 15
US-09-949-016-11880
/ Sequence 11880, Application US/09949016
/ Patent No. 681239
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11880
/ LENGTH: 174318
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(174318)
/ OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11880

```

Query Match	76.4%	Score 16.8;	DB 3;	Length 174318;
Best Local Similarity	65.0%;	Pred. NO. 2.5e+02;		
Matches 13;	Conservative 5;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 UAGCAGCACUAUAGCGUUG 20  
:|||||||:|:|  
Db 56520 TAGCAGCACATAATGCTATG 56539

Search completed: November 1, 2006, 22:24:17  
Job time : 44.1333 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 22:20:01 ; Search time 527.371 Seconds  
(without alignments)  
512.595 Million cell updates/sec

Title: US-10-706-798-3

Perfect score: 1 uagcagcacaauauguuug 22

Sequence: 1 uagcagcacaauauguuug 22

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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3: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US09\_PUBCOMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
11: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
12: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
13: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11B\_PUBCOMB.seq:\*  
14: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11C\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11D\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/US11E\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	8	US-10-706-798-3
2	22	100.0	22	10	US-10-490-955-81
3	22	100.0	22	10	US-10-490-955-119
4	22	100.0	22	10	US-10-490-955-448
5	22	100.0	22	10	US-10-740-256A-62
6	22	100.0	22	10	US-10-909-125-269
7	22	100.0	22	10	US-10-909-125-369
8	22	100.0	22	11	US-10-881-3628-7
9	22	100.0	22	15	US-11-055-035-16
10	22	100.0	22	15	US-11-102-453-15
11	22	100.0	22	15	US-11-102-453-111
12	22	100.0	22	15	US-11-100-897-5
13	22	100.0	22	15	US-11-100-897-7
14	22	100.0	22	15	US-11-100-897-73
15	22	100.0	22	16	US-11-171-175-131
16	22	100.0	27	10	US-10-909-125-887
17	22	100.0	70	10	US-10-909-125-1316

18	22	100.0	83	8	US-10-706-798-1	Sequence 1, Appli
19	22	100.0	83	10	US-10-490-955-248	Sequence 248, App
20	22	100.0	83	10	US-10-490-955-305	Sequence 305, App
21	22	100.0	83	15	US-11-100-897-72	Sequence 72, Appli
22	22	100.0	83	16	US-11-230-992-1	Sequence 1, Appli
23	22	100.0	110	10	US-10-909-125-128	Sequence 128, App
24	22	100.0	110	10	US-10-909-125-165	Sequence 165, App
25	22	100.0	310	10	US-10-909-125-906	Sequence 906, App
26	21	95.5	21	10	US-10-490-955-119	Sequence 19, Appli
27	21	95.5	21	10	US-10-909-125-1151	Sequence 1151, Ap
28	21	95.5	21	10	US-10-909-125-1768	Sequence 1768, Ap
29	20	90.9	22	10	US-10-708-204-23	Sequence 23, Appli
30	20	90.9	74	10	US-10-708-204-6357	Sequence 6357, Ap
31	20	90.9	76	10	US-10-708-204-6769	Sequence 6769, Ap
32	18.8	85.5	600	10	US-10-972-079-77545	Sequence 77545, A
33	18	81.8	23	8	US-10-706-798-5	Sequence 5, Appli
34	17.4	79.1	21	10	US-10-909-125-1115	Sequence 1115, Ap
35	17.4	79.1	21	10	US-10-909-125-1886	Sequence 1886, Ap
36	17.4	79.1	22	10	US-10-490-955-120	Sequence 120, App
37	17.4	79.1	22	10	US-10-490-955-449	Sequence 449, App
38	17.4	79.1	22	10	US-10-909-125-246	Sequence 246, App
39	17.4	79.1	22	15	US-10-909-125-345	Sequence 345, App
40	17.4	79.1	22	15	US-11-102-453-112	Sequence 112, App
41	17.4	79.1	22	16	US-11-171-175-132	Sequence 132, App
42	17.4	79.1	64	10	US-10-490-955-306	Sequence 306, App
43	17.4	79.1	85	10	US-10-909-125-1286	Sequence 1286, Ap
44	17.4	79.1	98	16	US-11-230-992-2	Sequence 2, Appli
45	17.4	79.1	110	10	US-10-909-125-80	Sequence 80, Appli

## ALIGNMENTS

RESULT 1  
US-10-706-798-3  
; Sequence 3, Application US/10706798  
; Publication No. US20040152112A1  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; TITLE OF INVENTION: Compositions and Methods for Cancer  
; FILE REFERENCE: 08321-0126US1  
; CURRENT APPLICATION NUMBER: US/10/706,798  
; CURRENT FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: 60/425,864  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/469,464  
; PRIOR FILING DATE: 2003-05-09  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-706-798-3  
Query Match 100.0%; Score 22; DB 8; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 UAGCAGCACAUAUGUUGUG 22  
Db 1 UAGCAGCACAUAUGUUGUG 22  
RESULT 2  
US-10-490-955-81  
; Sequence 81, Application US/10490955  
; Publication No. US2005005905A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuchi, Thomas  
; APPLICANT: Lagos-Quintana, Mariana

```
; APPLICANT: Lendeckel, Winfried
; APPLICANT: Meyer, Jutta
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-490-955-81
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Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 UAGCAGCACAUAAUGGUGUG 22
Db 1 UAGCAGCACAUAAUGGUGUG 22
```

```
RESULT 3
US-10-490-955-119
; Sequence 119, Application US/10490955
; Publication No. US20050059005A1
; GENERAL INFORMATION:
; APPLICANT: Tuschl, Thomas
; APPLICANT: Lendeckel, Winfried
; APPLICANT: Meyer, Jutta
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-490-955-119
```

```
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 UAGCAGCACAUAAUGGUGUG 22
Db 1 UAGCAGCACAUAAUGGUGUG 22
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```
RESULT 4
US-10-490-955-448
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; Sequence 448, Application US/10490955
; Publication No. US20050059005A1
; GENERAL INFORMATION:
; APPLICANT: Tuschl, Thomas
; APPLICANT: Lagos-Quintana, Mariana
; APPLICANT: Lendeckel, Winfried
; APPLICANT: Meyer, Jutta
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 448
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: D. melanogaster or H. sapiens or M. musculus or C. elegans or
US-10-490-955-448
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```
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 UAGCAGCACAUAAUGGUGUG 22
Db 1 UAGCAGCACAUAAUGGUGUG 22
```

```
RESULT 5
US-10-740-256A-62
; Sequence 62, Application US/10740256A
; Publication No. US20050074788A1
; GENERAL INFORMATION:
; APPLICANT: Dahlberg, James E.
; APPLICANT: Allawi, Hatim T.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson-Munoz, Marilyn
; APPLICANT: Chehak, LuAnne
; APPLICANT: Olson, Sarah M.
; TITLE OF INVENTION: Detection of Small Nucleic Acids
; FILE REFERENCE: FORS-08497
; CURRENT APPLICATION NUMBER: US/10/740,256A
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: modified_base
; LOCATION: (1)..(22)
; OTHER INFORMATION: 2'-O-methyl
US-10-740-256A-62
```

```
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1 UAGCAGCACAUAAUGGUGUUGG	22
Db	1 UAGCAGCACAUAAUGGUGUUGG	22

## RESULT 6

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US-10-909-125-269
? Sequence 269: Application US/10909125
? Publication No. US20050261218A1
? GENERAL INFORMATION:
? APPLICANT: Essau, Christine
? APPLICANT: Lollo, Bridget
? APPLICANT: Bennett, C. Frank
? APPLICANT: Freier, Susan M.
? APPLICANT: Grifley, Richard H.
? APPLICANT: Baker, Brenda F.
? APPLICANT: Vickers, Timothy
? APPLICANT: Marcusson, Eric G.
? APPLICANT: Koller, Erich
? APPLICANT: Swayze, Eric
? APPLICANT: Jain, Ravi
? APPLICANT: Bhat, Balkrishen
? APPLICANT: Peralta, Eigen
? TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
? FILE REFERENCE: IS1S0080-100 (CORE0016US)
? CURRENT APPLICATION NUMBER: US/10/909,125
? PRIOR FILING DATE: 2004-07-30
? PRIOR APPLICATION NUMBER: US 60/492,056
? PRIOR FILING DATE: 2003-07-31
? PRIOR APPLICATION NUMBER: US 60/516,303
? PRIOR FILING DATE: 2003-10-31
? PRIOR APPLICATION NUMBER: US 60/531,536
? PRIOR FILING DATE: 2003-12-19
? PRIOR APPLICATION NUMBER: US 60/562,417
? PRIOR FILING DATE: 2004-04-14
? NUMBER OF SEQ ID NOS: 2184
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 269
? LENGTH: 22
? TYPE: RNA
? ORGANISM: H. sapiens
US-10-909-125-269

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Query Match	100.0%	Score 22:	DB 10;	Length 22;
Best Local Similarity	100.0%	Pred. NC. 1.9;		
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY		1 UAGCAGCAUAAUGGUTTUGG	22
Dδ	1	UAGCAGCAUAAGAUGGUUGG	22

## RESULT 7

```

US-10-909-125-369/c
: Sequence 369, Application US/10909125
: Publication No. US20050261218A1
: GENERAL INFORMATION:
: APPLICANT: Esau, Christine
: APPLICANT: Lollo, Bridget
: APPLICANT: Bennett, C. Frank
: APPLICANT: Freier, Susan M.
: APPLICANT: Griffeey, Richard H.
: APPLICANT: Baker, Brenda F.
: APPLICANT: Vickers, Timothy
: APPLICANT: Marcussen, Eric G.
: APPLICANT: Koller, Erich
: APPLICANT: Swayze, Eric
: APPLICANT: Uain, Kavi
: APPLICANT: Bhat, BalKrishen
: APPLICANT: Petalita, Eigen
: TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation

```

```

; TITLE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30

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Query Match	100.0%	Score 22	DB 10	Length 22
Best Local Similarity	68.2%	Pred. No. 1	9	
Matches 15	Conservative 7	Mismatches 0	Indels 0	Gaps 0

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QY      1 UAGCAGCACAUAAUGGUGUUUG 22
      :|||:|||:|||:|||:|||:|
DB      22 TAGCAGCACATAATGGTTGTG 1

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## RESULT & DISCUSSION

```

1 : Sequence 7, Application US/10881.362B
2 : Publication No. US20060003337A1
3 :
4 : GENERAL INFORMATION:
5 :
6 : APPLICANT: Applied Biosystems
7 : TITLE OF INVENTION: Detection of Small RNAs
8 : FILE REFERENCE: 9692-000046
9 : CURRENT APPLICATION NUMBER: US/10/881.362B
10 : CURRENT FILING DATE: 2004-06-30
11 : NUMBER OF SEQ ID NOS: 43
12 :
13 : SOFTWARE: Patentin version 3.3
14 :
15 : SEQ ID NO 7
16 :
17 : LENGTH: 22
18 :
19 : TYPE: RNA
20 :
21 : ORGANISM: Human
22 :
23 : US-10-881-362B-7

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Query Match	100.0%;	Score 22;	DB 11;	Length 22;
Best Local Similarity	100.0%;	Pred. No. 1.9;		
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1 UAGCAGCACAUAAUGGUTUUG	22
D8	1 UAGCAGCACAUAAUGGUTUUG	22

## RESULT 5

US-11-055-035-16  
; Sequence 16, Application US/11055035  
; Publication No. US20050256072A1  
; GENERAL INFORMATION:  
; APPLICANT: ARONIN, NEIL  
; APPLICANT: ZAMORE, PHILLIP D.  
; APPLICANT: BRODEURICK, JENNIFER  
; TITLE OF INVENTION: DUAL FUNCTIONAL OLIGONUCLEOTIDES FOR USE IN REPRESSING  
; FILE REFERENCE: UMY-095  
; CURRENT APPLICATION NUMBER: US/11/055,035  
; CURRENT FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: 60/543,467  
; PRIOR FILING DATE: 2004-02-09

NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 16  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-055-035-16

Query Match 100.0%; Score 22; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCAUAUAGUGUUG 22  
DB 1 UAGCAGCAUAUAGUGUUG 22

RESULT 10  
US-11-102-453-15  
Sequence 15, Application US/11102453  
Publication No. US20050260648A1  
GENERAL INFORMATION:  
APPLICANT: Van Hufel, Christophe  
APPLICANT: Remacle, Jose  
APPLICANT: Bulow, Sven  
TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR  
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION  
FILE REFERENCE: KLAUS2.006CPI  
CURRENT APPLICATION NUMBER: US/11/102,453  
CURRENT FILING DATE: 2005-04-08  
PRIOR APPLICATION NUMBER: US 10/818,956  
PRIOR FILING DATE: 2004-04-06  
NUMBER OF SEQ ID NOS: 222  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-102-453-15

Query Match 100.0%; Score 22; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCAUAUAGUGUUG 22  
DB 1 UAGCAGCAUAUAGUGUUG 22

RESULT 11  
US-11-102-453-111  
Sequence 111, Application US/11102453  
Publication No. US20050260648A1  
GENERAL INFORMATION:  
APPLICANT: Van Hufel, Christophe  
APPLICANT: Remacle, Jose  
APPLICANT: Bulow, Sven  
APPLICANT: Zammatteo, Nathalie  
TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR  
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION  
FILE REFERENCE: KLAUS2.006CPI  
CURRENT APPLICATION NUMBER: US/11/102,453  
CURRENT FILING DATE: 2005-04-08  
PRIOR APPLICATION NUMBER: US 10/818,956  
PRIOR FILING DATE: 2004-04-06  
NUMBER OF SEQ ID NOS: 222  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 111  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Mus musculus  
US-11-102-453-111

Query Match 100.0%; Score 22; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCAUAUAGUGUUG 22  
DB 1 UAGCAGCAUAUAGUGUUG 22

RESULT 12  
US-11-100-897-5  
Sequence 5, Application US/11100897  
Publication No. US20050272075A1  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, Nana  
APPLICANT: Kongsbak, Lars  
APPLICANT: Kauppinen, Sakari  
APPLICANT: Echwald, Soren Morgenthaler  
APPLICANT: Mouritzen, Peter  
APPLICANT: Nielsen, Peter Stein  
APPLICANT: Notholm, Mikkel  
TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF MICRORNAs AND SMALL  
TITLE OF INVENTION: INTERFERING RNAs  
FILE REFERENCE: 50287/013004  
CURRENT APPLICATION NUMBER: US/11/100,897  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/648,221  
PRIOR FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: 60/619,291  
PRIOR FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: 60/600,961  
PRIOR FILING DATE: 2004-08-12  
PRIOR APPLICATION NUMBER: 60/590,856  
PRIOR FILING DATE: 2004-07-23  
PRIOR APPLICATION NUMBER: 60/560,148  
PRIOR FILING DATE: 2004-04-07  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5  
LENGTH: 22  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic sequence  
US-11-100-897-5

Query Match 100.0%; Score 22; DB 15; Length 22;  
Best Local Similarity 68.2%; Pred. No. 1.9;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCAUAUAGUGUUG 22  
DB 1 TAGCAGCAUATAGCTTGTG 22

RESULT 13  
US-11-100-897-7  
Sequence 7, Application US/11100897  
Publication No. US20050272075A1  
GENERAL INFORMATION:  
APPLICANT: Jacobsen, Nana  
APPLICANT: Kongsbak, Lars  
APPLICANT: Kauppinen, Sakari  
APPLICANT: Echwald, Soren Morgenthaler  
APPLICANT: Mouritzen, Peter  
APPLICANT: Nielsen, Peter Stein  
APPLICANT: Notholm, Mikkel  
TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF MICRORNAs AND SMALL  
TITLE OF INVENTION: INTERFERING RNAs  
FILE REFERENCE: 50287/013004  
CURRENT APPLICATION NUMBER: US/11/100,897  
CURRENT FILING DATE: 2005-04-07

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;;
; PRIOR APPLICATION NUMBER: 60/648,221
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 60/619,291
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/600,961
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/590,856
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/560,148
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 22
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-11-100-897-7
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Query Match          100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 UAGCAGACAUAAUGGUGUG 22
Db      1 UAGCAGACAUAAUGGUGUG 22
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RESULT 14
US-11-100-897-73
; Sequence 73, Application US/11100897
; Publication No. US20050272075A1
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, Nana
; APPLICANT: Kongsbak, Lars
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Echwald, Soren Morgenthaler
; APPLICANT: Mouritzen, Peter
; APPLICANT: Nielsen, Peter Stein
; APPLICANT: Norholm, Mikkel
; TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF MICRORNAs AND SMALL
; FILE REFERENCE: 50287/013004
; CURRENT APPLICATION NUMBER: US/11/100,897
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/648,221
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 60/619,291
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/600,961
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/590,856
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/560,148
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-100-897-73
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Query Match          100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 UAGCAGACAUAAUGGUGUG 22
Db      1 UAGCAGACAUAAUGGUGUG 22
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RESULT 15
US-11-171-175-131/c
; Sequence 131, Application US/11171175
; Publication No. US20060019286A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Miska, Eric A.
; APPLICANT: Alvarez-Saavedra, Ezequiel A.
; TITLE OF INVENTION: High Throughput Methods Relating to MicroRNA Expression Analysis
; FILE REFERENCE: 01997/554003
; CURRENT APPLICATION NUMBER: US/11/171,175
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/607,531
; PRIOR FILING DATE: 2004-09-07
; PRIOR APPLICATION NUMBER: 60/584,381
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-171-175-131
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Query Match          100.0%; Score 22; DB 16; Length 22;
Best Local Similarity 68.2%; Pred. No. 1.9;
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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Db      22 TAGCAGACATATGTTGTG 1
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Job time : 528.371 secs
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OM nucleic - nucleic search, using sw model

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859.641 Million cell updates/sec

Title: US-10-706-798-3

Perfect score: 22  
Sequence: 1 uacgacgacacauaugguugug 22

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Gapop 10.0 , Gapext 1.0

Searched: 2461376 seqs, 970166171 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	US-10-818-956-15	Sequence 15, Appl
2	22	100.0	22	US-10-818-956-111	Sequence 111, Appl
3	22	100.0	22	US-11-317-660-36	Sequence 36, Appl
4	22	100.0	22	US-11-317-660-795	Sequence 795, Appl
5	22	100.0	22	US-11-084-082-2	Sequence 2, Appl
6	22	100.0	22	US-11-084-082-27	Sequence 27, Appl
7	22	100.0	22	US-11-242-139-31	Sequence 31, Appl
8	22	100.0	22	US-11-242-139-127	Sequence 127, Appl
9	22	100.0	22	US-11-375-650-3	Sequence 3, Appl
10	22	100.0	40	US-11-194-055-325	Sequence 325, Appl
11	22	100.0	78	US-11-084-082-26	Sequence 26, Appl
12	22	100.0	83	US-11-194-055-33	Sequence 33, Appl
13	22	100.0	83	US-11-375-650-1	Sequence 1, Appl
14	22	100.0	108	US-11-194-055-32	Sequence 32, Appl
15	22	100.0	347503	US-11-266-748A-23474	Sequence 23474, A
16	18.8	85.5	7808	US-10-959-175-4	Sequence 4, Appl
17	18.8	85.5	7824	US-10-959-175-5	Sequence 5, Appl
18	18	81.8	23	US-11-375-650-5	Sequence 5, Appl
19	17.8	80.9	1200	US-11-266-748A-302054	Sequence 302054, A
20	17.4	79.1	22	US-10-818-956-112	Sequence 112, Appl
21	17.4	79.1	22	US-11-317-660-37	Sequence 37, Appl
22	17.4	79.1	22	US-11-317-660-796	Sequence 796, Appl
23	17.4	79.1	22	US-11-242-139-128	Sequence 128, Appl

24	17.4	79.1	40	US-11-194-055-327	Sequence 327, Appl
25	17.4	79.1	64	US-11-194-055-34	Sequence 34, Appl
26	17.4	79.1	98	US-11-194-055-35	Sequence 35, Appl
27	17.2	78.2	132	US-11-266-748A-119432	Sequence 119432, A
28	16.4	74.5	1000	US-11-266-748A-221650	Sequence 221650, A
29	16.4	74.5	1000	US-11-266-748A-286791	Sequence 286791, A
30	16.4	74.5	1000	US-11-266-748A-338220	Sequence 338220, A
31	16.4	74.5	1000	US-11-266-748A-397338	Sequence 397338, A
32	16.4	74.5	1000	US-11-266-748A-468384	Sequence 468384, A
33	16.4	74.5	34161	US-10-539-228-436	Sequence 436, Appl
34	16.4	74.5	43179	US-10-539-228-383	Sequence 383, Appl
35	16.2	73.6	201	US-10-284-444-12515	Sequence 12515, A
36	16.2	73.6	201	US-10-284-444-12517	Sequence 12517, A
37	16.2	73.6	335	US-11-244-330A-2226	Sequence 2226, Appl
38	16.2	73.6	493	US-11-266-748A-100416	Sequence 100416, A
39	16.2	73.6	493	US-11-266-748A-153227	Sequence 153227, A
40	16.2	73.6	585	US-10-471-571A-2965	Sequence 2965, Appl
41	16.2	73.6	664	US-11-266-748A-299464	Sequence 299464, A
42	16.2	73.6	879	US-11-266-748A-91874	Sequence 91874, A
43	16.2	73.6	879	US-11-266-748A-144685	Sequence 144685, A
44	16.2	73.6	916	US-11-266-748A-48314	Sequence 48314, A
45	16.2	73.6	1000	US-11-266-748A-224816	Sequence 224816, A

# ALIGNMENTS

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RESULT 1
US-10-818-956-15
; Sequence 15, Application US/10818956
; Publication No. US20060134639A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR
; FILE REFERENCE: KLAUS2.006AUS
; CURRENT APPLICATION NUMBER: US/10/818,956
; CURRENT FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-818-956-15

Query Match      100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 UACGACGACAUAAUGGUGUGUG 22
Db      1 UACGACGACAUAAUGGUGUGUG 22

RESULT 2
US-10-818-956-111
; Sequence 111, Application US/10818956
; Publication No. US20060134639A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR
; FILE REFERENCE: KLAUS2.006AUS
; CURRENT APPLICATION NUMBER: US/10/818,956
; CURRENT FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 212

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: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 111
: LENGTH: 22
: TYPE: RNA
: ORGANISM: Mus musculus
US-10-818-956-111

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Query Match      100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 UAGCAGCACAUAAUGGUTUGUG 22
         |||||
Db      1 UAGCAGCACAUAAUGGUTUGUG 22

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RESULT 3  
US-11-317-660-36

APPLICANT: BARTEL, DAVID P.  
APPLICANT: JONES-RHOADES, MATTHEW W.

```

; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING MIRNA TARGETS
;
; TITLE OF INVENTION: AND FOR ALTERING MIRNA AND TARGET EXPRESSION
;
; FILE REFERENCE: W0571.70013US01
;

```

; PRIOR APPLICATION NUMBER: 60/639,231  
 ; PRIOR FILING DATE: 2004-12-23  
 ; NUMBER OF SEQ ID NOS: 1227

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; ORGANISM: Artificial Sequence
;
; TYPE: RNA
;
; LENGTH: 22
;
; ORIGIN:

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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; OTHER INFORMATION: oligonucleotide
US-11-317-660-36

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Query Match	100.0%	Score 22;	DB 7;	Length 22;
Best Local Similarity	100.0%	Pred. No. 0.093;		
Matches 22; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 UAGCAGCACAUAUUGGUTUGG 22  
|||  
Db 1 UAGCAGCACAUAUUGGUTUGG 22

RESULT 4  
US-11-317-660-795/c

```

;
; GENERAL INFORMATION:
;
; APPLICANT: BARTEL, DAVID P.
;
; APPLICANT: JONES-RHOADES, MATTHEW W.

```

FILE REFERENCE: W0571.70013US01

NUMBER OF SEQ ID NOS: 1227  
PRIOR FILING DATE: 2004-12-23  
PRIOR APPLICATION NUMBER: 60/639,231  
CURRENT FILING DATE: 2005-12-23

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; SEQ ID NO 795
; LENGTH: 22
; TYPE: RNA

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? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
? OTHER INFORMATION: oligonucleotide
US-11-317-660-795

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Query Match	100.0%	Score 22	DB 7	Length 22
Best Local Similarity	68.2%	Pred. No. 0.093		
Matches 15	Conservative 7	Mismatches 0	Indels 0	Gaps 0

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QY      1 UAGCAGCACUAAGUGGUGG 22
      :|||||||:|:|:|:|:|:|
Db      22 TAGCAGCACATAATGCTTGTG 1

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RESULT 5  
US-11-084-082-2  
; Sequence 2, Application US/11084082

APPLICANT: SORGE, JOSEPH A.  
APPLICANT: MULLINAX, REBECCA L.  
TITLE OF INVENTION: METHODS, COMPOSITIONS, AND KITS FOR DETECTION OF

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; CURRENT APPLICATION NUMBER: US/11/084,082
; CURRENT FILING DATE: 2005-03-21
; NUMBER OF SEQ ID NOS: 41

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;
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence

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OTHER INFORMATION: description of material received: *Syntherisma*  
; OTHER INFORMATION: oligonucleotide  
US-11-084-082-2

Best Local Similarity	100.0%	Pred. NO.	0.093						
Matches	22	Conservative	0	Mismatches	0	Indels	0	Gaps	0

1 UAGCAGCACAUAAUGGUGUUG 22

US-11-084-082-27  
; Sequence 27, Application US/11084082  
; Publication No. US20060211000A1

APPLICANT: SORGE, JOSEPH A.  
APPLICANT: MULLINX, REBECCA L.  
TITLE OF INVENTION: METHODS, COMPOSITIONS, AND KITS FOR DETECTION OF  
TITLE OF INVENTION: MICRORNA

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; CURRENT APPLICATION NUMBER: US/11/084,082
; CURRENT FILING DATE: 2005-03-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin ver 3.3

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; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence

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OTHER INFORMATION: oligonucleotide  
US-11-084-082-27

Query Match	100.0%	Score 42	15	Length 22
Query Local Similarity	100.0%	Pred. No. 0.093		
Matches 22; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;



Qy 1 UAGCAGCACAUAAUGGUGUG 22  
Db 1 UAGCAGCACAUAAUGGUGUG 22

RESULT 7  
US-11-242-139-31

; Sequence 31, Application US/11242139  
; Publication No. US20060099619A1  
; GENERAL INFORMATION:  
; APPLICANT: REMACLE, JOSE  
; APPLICANT: DU LONGUEVILLE, FRANCOISE  
; APPLICANT: HAMELS, SANDRINE  
; TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF MIRNA ON MICRO-ARRAYS  
; FILE REFERENCE: 035642-0107  
; CURRENT FILING DATE: 2005-10-04  
; PRIOR APPLICATION NUMBER: 10/637,656  
; PRIOR FILING DATE: 2003-08-11  
; NUMBER OF SEQ ID NOS: 239  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 31  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-242-139-31

Query Match 100.0%; Score 22; DB 8; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.093;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUGUG 22  
Db 1 UAGCAGCACAUAAUGGUGUG 22

RESULT 8  
US-11-242-139-127

; Sequence 127, Application US/11242139  
; Publication No. US20060099619A1  
; GENERAL INFORMATION:  
; APPLICANT: REMACLE, JOSE  
; APPLICANT: DU LONGUEVILLE, FRANCOISE  
; APPLICANT: HAMELS, SANDRINE  
; TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF MIRNA ON MICRO-ARRAYS  
; FILE REFERENCE: 035642-0107  
; CURRENT FILING DATE: 2005-10-04  
; PRIOR APPLICATION NUMBER: 10/637,656  
; PRIOR FILING DATE: 2003-08-11  
; NUMBER OF SEQ ID NOS: 239  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 127  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-11-242-139-127

Query Match 100.0%; Score 22; DB 8; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.093;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUGUG 22  
Db 1 UAGCAGCACAUAAUGGUGUG 22

RESULT 9  
US-11-375-650-3  
; Sequence 3, Application US/11375650  
; Publication No. US20060165659A1  
; GENERAL INFORMATION:

; APPLICANT: Croce, Carlo M.  
; APPLICANT: Calin, George A.  
; TITLE OF INVENTION: Compositions and Methods for Cancer  
; TITLE OF INVENTION: Diagnosis and Therapy  
; FILE REFERENCE: 08321-0126US1  
; CURRENT APPLICATION NUMBER: US/11/375,650  
; CURRENT FILING DATE: 2006-03-13  
; PRIOR APPLICATION NUMBER: US/10/706,798  
; PRIOR FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: 60/425,864  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/469,464  
; PRIOR FILING DATE: 2003-05-09  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-375-650-3

Query Match 100.0%; Score 22; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.093;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUGUG 22  
Db 1 UAGCAGCACAUAAUGGUGUG 22

RESULT 10  
US-11-194-055-325

; Sequence 325, Application US/11194055  
; Publication No. US20060105360A1  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; APPLICANT: Lin, Chang-Gong  
; APPLICANT: Calin, George A.  
; APPLICANT: Cinzia, Sevignani  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH  
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL  
; TITLE OF INVENTION: FEATURES  
; FILE REFERENCE: 3589.1018-008  
; CURRENT APPLICATION NUMBER: US/11/194,055  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: PCT/US2005/004865  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: 60/543,119  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,929  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,963  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,940  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/580,959  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 60/580,797  
; PRIOR FILING DATE: 2004-06-18  
; NUMBER OF SEQ ID NOS: 663  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 325  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide probe  
US-11-194-055-325

Query Match 100.0%; Score 22; DB 8; Length 40;  
Best Local Similarity 68.2%; Pred. No. 0.1;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGACAUAAUGGUGUG 22  
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Db 14 TAGCAGACATTAATGCTTTGTG 35

RESULT 11  
US-11-084-082-26/c  
; Sequence 26, Application US/11084082  
; Publication No. US20060211000A1  
; GENERAL INFORMATION:  
; APPLICANT: SORGE, JOSEPH A.  
; APPLICANT: MULLENX, REBECCA L.  
; TITLE OF INVENTION: METHODS, COMPOSITIONS, AND KITS FOR DETECTION OF  
; TITLE OF INVENTION: MICRORNA  
; FILE REFERENCE: STG-114  
; CURRENT APPLICATION NUMBER: US/11/084,082  
; CURRENT FILING DATE: 2005-03-21  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 26  
; LENGTH: 78  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-084-082-26

Query Match 100.0%; Score 22; DB 7; Length 78;  
Best Local Similarity 68.2%; Pred. No. 0.11;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGACAUAAUGGUGUG 22  
:|||||:|||||:  
Db 49 TAGCAGACATTAATGCTTTGTG 28

RESULT 12  
US-11-194-055-33  
; Sequence 33, Application US/11194055  
; Publication No. US20060105360A1  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; APPLICANT: Liu, Chang-Gong  
; APPLICANT: Cincia, Sevianni  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH  
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL  
; FILE REFERENCE: 3589.1018-008  
; CURRENT APPLICATION NUMBER: US/11/194,055  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: PCT/US2005/004865  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: 60/543,119  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,929  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,963  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,940  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/580,959  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 60/580,797  
; PRIOR FILING DATE: 2004-06-18  
; NUMBER OF SEQ ID NOS: 663  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 83  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-194-055-33

Query Match 100.0%; Score 22; DB 8; Length 83;  
Best Local Similarity 68.2%; Pred. No. 0.11;  
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGACAUAAUGGUGUG 22  
:|||||:|||||:  
Db 14 TAGCAGACATTAATGCTTTGTG 35

RESULT 13  
US-11-375-650-1  
; Sequence 1, Application US/11375650  
; Publication No. US20060165659A1  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; APPLICANT: Cincia, Sevianni  
; TITLE OF INVENTION: Compositions and Methods for Cancer  
; TITLE OF INVENTION: Diagnosis and Therapy  
; FILE REFERENCE: 08321-0126US1  
; CURRENT APPLICATION NUMBER: US/11/375,650  
; CURRENT FILING DATE: 2006-03-13  
; PRIOR APPLICATION NUMBER: US/10/706,798  
; PRIOR FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: 60/425,864  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/469,464  
; PRIOR FILING DATE: 2003-05-09  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 83  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-375-650-1

Query Match 100.0%; Score 22; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGACAUAAUGGUGUG 22  
:|||||:|||||:  
Db 14 UAGCAGACAUAAUGGUGUG 35

RESULT 14  
US-11-194-055-32  
; Sequence 32, Application US/11194055  
; Publication No. US20060105360A1  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo M.  
; APPLICANT: Liu, Chang-Gong  
; APPLICANT: Cincia, Sevianni  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH  
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL  
; FILE REFERENCE: 3589.1018-008  
; CURRENT APPLICATION NUMBER: US/11/194,055  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: PCT/US2005/004865  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: 60/543,119  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,929  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,963  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/542,940  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: 60/580,959  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 60/580,797

, Thu Nov 2 10:08:17 2006

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; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-32
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Query Match          100.0%; Score 22; DB 8; Length 108;
Best Local Similarity 68.2%; Pred. No. 0.12;
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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QY      1 UAGCAGCACAUAVUGUUUG 22
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Db      43 TAGCAGCACATATAGTTGTG 64
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RESULT 15
US-11-266-748A-23474/c
; Sequence 23474, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23474
; LENGTH: 347503
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23474
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Query Match          100.0%; Score 22; DB 8; Length 347503;
Best Local Similarity 68.2%; Pred. No. 0.41;
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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QY      1 UAGCAGCACAUAVUGUUUG 22
      :|||||:|:|:|:|:|
Db      52185 TAGCAGCACATATAGTTGTG 52164
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Search completed: November 1, 2006, 22:36:58
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